

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:19:12 ; Search time 12.3158 Seconds
(without alignments)
710.580 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539
Sequence: 1 KSPVVDCHGDRSYRGIS.....DPCRWBYCNLTQCSRTESG 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	539	100.0	4548	1 S00657	apoprotein(a) (EC
2	535	95.5	1420	2 A32869	apoliipoprotein(a)
3	455	78.8	810	2 B30848	plasma (EC 3.4.21
4	423	78.5	810	1 PLHU	plasma (EC 3.4.21
5	413	76.6	812	1 PLBO	plasma (EC 3.4.21
6	405	75.1	123	2 C61545	plasma (EC 3.4.21
7	402	74.6	790	1 PLRG	plasma (EC 3.4.21
8	388	72.0	812	1 PLMS	plasma (EC 3.4.21
9	387	71.8	455	2 A61545	plasma (EC 3.4.21
10	387	71.8	460	2 B61545	plasma (EC 3.4.21
11	384	71.2	120	2 E61545	plasma (EC 3.4.21
12	378	70.1	810	2 I46260	plasma (EC 3.4.21
13	363.5	67.4	169	2 A40522	plasma (EC 3.4.21
14	359	61.0	89	2 A60140	plasma (EC 3.4.21
15	281	52.1	2869	2 T18518	apoliipoprotein(a)
16	255	47.3	728	1 JH0579	hepatocyte growth
17	250.5	46.5	710	1 I51283	hepatocyte growth
18	250	46.4	728	1 A35644	hepatocyte growth
19	249.5	46.3	946	1 A47299	hepatocyte growth
20	249	46.2	728	1 A60185	hepatocyte growth
21	241.5	44.8	716	1 A40332	hepatocyte growth
22	238.5	44.2	716	1 JCS061	hepatocyte growth
23	232	43.0	411	2 I51285	hepatocyte growth
24	231.5	42.9	711	1 A47136	hepatocyte growth
25	204	37.8	336	2 S33879	plasma precursor
26	201.5	37.4	622	1 TBHU	chromin (EC 3.4.2
27	200.5	37.2	943	2 B45082	neurotrophic recep
28	200	37.1	617	2 S10511	chromin (EC 3.4.2
29	196	36.4	618	2 A35827	chromin (EC 3.4.2

30	193.5	35.9	625	1 TBHO	thrombin (EC 3.4.2
31	190.5	35.3	560	1 JC4795	plasma hyaluronan-
32	189.5	35.2	937	2 A45082	neurotrophic recep
33	186	34.5	562	1 UKRUT	t-plasminogen acti
34	181.5	33.7	603	2 S28941	coagulation factor
35	181.5	33.7	615	1 KFH12	plasma hyaluronan-
36	180.5	33.5	558	2 JC5878	t-plasminogen acti
37	176.5	32.7	559	1 A35029	coagulation factor
38	173.5	32.2	593	2 S45281	t-plasminogen acti
39	173	32.1	559	1 A29941	hepatocyte growth
40	173	32.1	655	1 A46688	hepatocyte growth
41	166	30.8	432	1 S18932	u-plasminogen acti
42	161	29.9	442	1 UKPG	u-plasminogen acti
43	157	29.1	433	1 UKMS	u-plasminogen acti
44	156	28.9	433	1 UN0560	u-plasminogen acti
45	148	27.5	433	1 UKRAY	u-plasminogen acti

ALIGNMENTS

RESULT 1
S00657
apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N/Alternate names: apoliipoprotein(a); lipoprotein(a) chain apo(a)
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 08-Dec-2000
C/Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R/McLean, J.W.; Tomlinson, J.E.; Kuang, W.-J.; Eaton, D.L.; Chen, E.Y.; Fleese, G.M.; Seam
Nature 330, 132-137, 1987
A/Title: cDNA sequence of human apoliipoprotein(a) is homologous to plasminogen.
A/Reference number: S00657; MUID:88039109; PMID:3670400
A/Accession: S00657
A/Molecule type: mRNA
A/Residues: 1-4548 <MCL>
A/Cross-References: GB:X06290; EMBL:X06696; NID:G28619; PIDN:CA29618.1; PID:G28620
R/Bacon, D.L.; Fleese, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.;
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A/Title: Partial amino acid sequence of apoliipoprotein(a) shows that it is homologous to
A/Reference number: A28017; MUID:87204109; PMID:3472206
A/Accession: A28017
A/Molecule type: protein
A/Residues: 20-21,'P',23-34,177-179,'N',181-186,'T',188-196,'DKG',200;292-314,'W',316-318
X',4396-4401 <EXT>
R/Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meier, K.; Schwartz, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A/Title: 5' control regions of the apoliipoprotein(a) gene and members of the related plas
A/Reference number: A47277; MUID:93165698; PMID:7679504
A/Accession: A47277
A/Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RES>
A/Cross-References: GB:L07899; NID:G967973; PID:G967974
R/Magaret, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacor
Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A/Title: Characterization of yeast artificial chromosome cloning of the linked apoliipop
A/Reference number: A47233; MUID:93087573; PMID:1454851
A/Accession: A47233
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-16 <RES>
A/Molecule type: DNA
A/Cross-References: GB:M60078; NID:G178786; PIDN:AAA5547.1; PID:G553188
A/Note: apo(a) gene 1 (nomenclature of reference I52415)
A/Accession: A47233
A/Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RES>
A/Cross-References: GB:M60079; NID:G178784; PIDN:AAA5546.1; PID:G553187
R/Chinose, A.
Biochemistry 31, 3113-3118, 1992
A/Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated wit
A/Reference number: I52415; MUID:92207924; PMID:1554698
A/Accession: I52415

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <KR>
A:Cross-references: GB:M86877; NID:g178780; PIDN:AAA9909.1; PID:g553185
A:Note: apo(a) gene 1 (nomenclature of reference 152415)
A:Accession: 165286
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <KR>
A:Cross-references: GB:M86878; NID:g178782; PIDN:AAA51749.1; PID:g553186
A:Gene: GDB:LPA
A:Cross-references: GDB:120699; OMIM:152200
A:Map position: 6q26-6q27
A:Note: several genes closely linked on chromosome 6 are identical in the first coding
re of kringle repeats
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-4548/Product: apolipoprotein(a) #status experimental <MAT>
F:28-105/Domain: kringle homology <KR1>
F:142-219/Domain: kringle homology <KR2>
F:256-333/Domain: kringle homology <KR3>
F:370-447/Domain: kringle homology <KR4>
F:484-561/Domain: kringle homology <KR5>
F:598-675/Domain: kringle homology <KR6>
F:712-789/Domain: kringle homology <KR7>
F:826-903/Domain: kringle homology <KR8>
F:940-1017/Domain: kringle homology <KR9>
F:1054-1131/Domain: kringle homology <KR10>
F:1168-1245/Domain: kringle homology <KR11>
F:1282-1359/Domain: kringle homology <KR12>
F:1396-1473/Domain: kringle homology <KR13>
F:1510-1587/Domain: kringle homology <KR14>
F:1624-1701/Domain: kringle homology <KR15>
F:1738-1815/Domain: kringle homology <KR16>
F:1852-1929/Domain: kringle homology <KR17>
F:1966-2043/Domain: kringle homology <KR18>
F:2080-2157/Domain: kringle homology <KR19>
F:2194-2271/Domain: kringle homology <KR20>
F:2308-2385/Domain: kringle homology <KR21>
F:2422-2499/Domain: kringle homology <KR22>
F:2536-2613/Domain: kringle homology <KR23>
F:2650-2727/Domain: kringle homology <KR24>
F:2764-2841/Domain: kringle homology <KR25>
F:2878-2955/Domain: kringle homology <KR26>
F:2992-3069/Domain: kringle homology <KR27>
F:3106-3183/Domain: kringle homology <KR28>
F:3220-3297/Domain: kringle homology <KR29>
F:3334-3411/Domain: kringle homology <KR30>
F:3448-3525/Domain: kringle homology <KR31>
F:3562-3639/Domain: kringle homology <KR32>
F:3676-3753/Domain: kringle homology <KR33>
F:3782-3859/Domain: kringle homology <KR34>
F:3896-3973/Domain: kringle homology <KR35>
F:4010-4087/Domain: kringle homology <KR36>
F:4124-4201/Domain: kringle homology <KR37>
F:4228-4307/Domain: kringle homology <KR38>
F:4328-4541/Domain: trypsin homology <TRY>
Query Match 100.0%; Score 539; DB 1; Length 4548;
Best Local Similarity 100.0%; Pred. No. 2, 4e-44;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
A32869
apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
C:Accession: A32869; A30848
R:Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A:Reference number: A32869; PMID:89174660; PMID:2925643
A:Accession: A32869
A:Molecule type: mRNA
A:Residues: 1-1420 <TOM>
A:Cross-references: GB:J04635; NID:g342072; PIDN:AAA6833.1; PID:g342073
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F:50-117/Domain: kringle homology <KR1>
F:164-241/Domain: kringle homology <KR2>
F:278-355/Domain: kringle homology <KR3>
F:392-469/Domain: kringle homology <KR4>
F:506-583/Domain: kringle homology <KR5>
F:620-697/Domain: kringle homology <KR6>
F:726-803/Domain: kringle homology <KR7>
F:840-917/Domain: kringle homology <KR8>
F:954-1031/Domain: kringle homology <KR9>
F:1068-1145/Domain: kringle homology <KR10>
F:1191-1413/Domain: trypsin homology <TRY>

Query Match 95.5%; Score 515; DB 2; Length 1420;
Best Local Similarity 94.5%; Pred. No. 1, 8e-42;
Matches 86; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KSPVDDCYHGDGRSIRGISSTVTGRTCSQSSMIPHHORTPENYPNAGLTENYCRNP 60
Db 947 KSPVDDCYHGDGRSIRGISSTVTGRTCSQSSMIPHHORTPENYPNAGLTENYCRNP 1006
Qy 61 DSGKQPCWCTTDPDPCVMEYCNLTQCSSTESG 91
Db 1007 DSGKHPWCCTTDPDPCVMEYCNLTQCSSTESG 1037

RESULT 3
B30848
plasmin (EC 3.4.21.7) precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C:Accession: B32869; B30848
J:Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A:Reference number: A32869; PMID:89174660; PMID:2925643
A:Accession: B32869
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-810 <TOM>
A:Cross-references: GB:J04697; NID:g342272; PIDN:AAA6901.1; PID:g342273
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-96/Domain: signal sequence #status predicted <SIG>
F:103-181/Domain: kringle homology <KR1>
F:185-262/Domain: kringle homology <KR2>
F:275-352/Domain: kringle homology <KR3>
F:377-454/Domain: kringle homology <KR4>
F:481-560/Domain: kringle homology <KR5>
F:581-603/Domain: trypsin homology <TRY>
F:49-73, 53-61, 103-181, 124-164, 152-176, 185-262, 188-316, 206-245, 234-257, 275-352, 296-335, 324-
bonds: #status predicted
F:622, 665, 760/Active site: His, Asp, Ser #status predicted
Query Match 78.8%; Score 425; DB 2; Length 810;
Best Local Similarity 77.3%; Pred. No. 6, 7e-34;
Matches 68; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 2 SPVDDQCHGAGCRSRYRGISSITTVTCRTGCOSSSMI PHHQRTPENYPAAGLTENYCENPD 61
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
DB 371 TPVVECTCHGGQSGYRGISSTTTTGCKCOSSSMTPHHMKTPENFPAALGNMYCRRNPD 430

QY 62 SGKOPWCYTTPDCVMEYECNLTQCEETE 89
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
DB 431 ADKGPWCFTTDPDSVMXEYCNLKKCSGTE 458

RESULT 4

PLHM
plasmin (BC 3.4.21.7) precursor [validated] - human
N.alternate names: plasminogen precursor [misnomer]
N.contains: angiotensin; microplasma; plasminogen
C.species: Homo sapiens (man)
C.date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 15-Sep-2000
A.accession: A55229; 152242; A26646; 162788; 184609; S03735; A00929; A04627; A04625; A04628;
J.Petersen, T.E.; Marzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265: 6104-6111, 1990
A.title: Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolysis system
A.reference number: A55229; PMID:9020879; PMID:2318848
A.accession: A55229
A.molecule type: DNA
A.residues: 1-810 <P&T>
A.cross-references: GB:M6286; GB:M34276; NID:g190064; PIDN:AAA60113.1; PID:g387026
A.experimental source: leukocyte; lung fibroblast
M.Margaretts, N.; Bruno, L.; Portogallo, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Tarantini, P.;
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A.title: Definition of the transcription initiation site of human plasminogen gene in lambda phage
A.reference number: 152242; PMID:91097523; PMID:2268308
A.accession: 152242
A.status: translated from GB/EMBL/DDBJ
A.molecule type: DNA
A.residues: 1-16 <MAL2>
A.cross-references: NID:g190092; PIDN:AAA6454.1; PID:g553613
R.Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A.title: Molecular cloning and characterization of a full-length cDNA clone for human plasminogen activator
A.reference number: A26646; PMID:87162490; PMID:3030813
A.accession: A26646
A.molecule type: mRNA
A.residues: 1-471, 'D', 473-810 <FOR>
A.cross-references: GB:X05199; NID:g35530; PIDN:CMA28831.1; PID:g35531
A.experimental source: liver
R.Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A.title: Characterization of a complementary deoxyribonucleic acid coding for human and rat plasminogen activator
A.reference number: 145961; PMID:8502311; PMID:6148961
A.accession: 162738
A.status: translated from GB/EMBL/DDBJ
A.molecule type: mRNA
A.residues: 292-471, 'D', 473-810 <MAL2>
A.cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031
A.accession: 184609
A.status: translated from GB/EMBL/DDBJ
A.molecule type: DNA
A.residues: 367-419 <MAL3>
A.cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
R.Brundish, R.A.; Lerch, P.G.; Schaller, U.; Rickli, E.E.; Lejter, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A.title: Comparison of the primary structure of the N-terminal CNBR fragments of human, rabbit, and bovine plasminogen activators
A.reference number: S03735; PMID:81212097; PMID:7238497
A.accession: S03735
A.molecule type: protein
A.residues: 20-71, 'E', 73-76 <BRU>
R.Sottrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A.reference number: A00929
A.accession: A00929
A.molecule type: protein
A.residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>
R.Wiman, B.

Eur. J. Biochem. 76, 129-137, 1977
 A>Title: Primary structure of the B-chain of human plasmin.
 A:Reference number: A04627; MUID:77225245; PMID:142009
 A:Accession: A04627
 A:Molecule type: protein
 A:Residues: 581-810 <W11>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 50, 489-494, 1975
 A>Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen.
 A:Reference number: A04625; MUID:75093329; PMID:122932
 A:Accession: A04625
 A:Molecule type: protein
 A:Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <W12>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 58, 539-547, 1975
 A>Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that contains the primary structure of the A-chain.
 A:Reference number: A04626; MUID:76043692; PMID:126863
 A:Accession: A04626
 A:Molecule type: protein
 A:Residues: 483-507, 'E', 509-604 <W13>
 R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summari, L.
 J. Biol. Chem. 248, 1631-1633, 1973
 A>Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen.
 A:Reference number: A82125; MUID:73149248; PMID:4694729
 A:Contents: annotation; active site
 R:Groskopf, W.R.; Summari, L.; Robbins, K.C.
 J. Biol. Chem. 244, 3590-3597, 1969
 A>Title: Studies on the active center of human plasmin.
 A:Reference number: A92048; MUID:69234739; PMID:4240117
 A:Contents: annotation; active site
 R:Trexler, M.; Vali, Z.; Patchy, L.
 J. Biol. Chem. 257, 7401-7406, 1982
 A>Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
 A:Reference number: A92382; MUID:82213905; PMID:6919539
 A:Contents: annotation; omega-aminocarboxylic acid binding sites
 R:Vali, Z.; Patchy, L.
 J. Biol. Chem. 259, 13690-13694, 1984
 A>Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin binding.
 A:Reference number: A92458; MUID:85054794; PMID:6094526
 A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
 R:Geo, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehnel, S.; Mccance, S.G.; J. Biol. Chem. 271, 29461-29467, 1996
 A>Title: Kring domains of human angiotensin. Characterization of the anti-proliferative activity of the kring domain.
 A:Reference number: A58811; MUID:97067211; PMID:8910613
 A:Contents: annotation
 R:Liljen, H.R.; Uegwi, F.; Bini, A.; Collen, D.
 Biochemistry 37, 4699-4702, 1998
 A>Title: Generation of an angiotensin-like fragment from plasminogen by streptolysin-1 (MS).
 A:Reference number: A58812; MUID:9548733; PMID:9548733
 A:Contents: annotation
 R:Tulinaky, A.; Mulichak, A.M.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51341; PDB:1PK4
 A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
 R:Tulinaky, A.; Wu, T.P.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51488; PDB:2PK4
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
 R:Wu, T.P.; Tulinaky, A.
 submitted to the Brookhaven Protein Data Bank, August 1993
 A:Reference number: A51911; PDB:1PKR
 A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
 R:Padmanabhan, K.; Tulinaky, A.
 submitted to the Brookhaven Protein Data Bank, April 1994
 A:Reference number: A52408; PDB:1PKK
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
 R:Tulinaky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995
 A:Reference number: A65244; PDB:1CEA
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 R:Tulinaky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995

A:Reference number: A65245; PDB:1CEB
 A:Content: annotation: X-ray crystallography, 2.1 angstroms, residues 102-181
 R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
 Biochemistry 30, 10576-10588, 1991
 A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 Å
 A:Reference number: A58819; PMID:1657148
 A:Content: annotation
 R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
 Biochemistry 30, 10589-10594, 1991
 A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
 A:Reference number: A58818; PMID:1657149
 A:Content: annotation
 R:de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.
 Biochemistry 31, 270-279, 1992
 A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.0 Å
 A:Reference number: A39483; PMID:1310033
 A:Content: annotation: X-ray crystallography, 2.4 angstroms
 R:Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
 submitted to the Brookhaven Protein Data Bank, June 1995
 A:Reference number: A65980; PDB:1KRN
 A:Content: annotation: X-ray crystallography, 1.67 angstroms, residues 376-454
 R:Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65803; PDB:1HPJ
 A:Content: annotation: conformation by (1)H-NMR, residues 103-181
 R:Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65804; PDB:1HPK
 A:Content: annotation: conformation by (1)H-NMR, residues 103-181
 R:Rejante, M.; Llinas, M.
 Eur. J. Biochem. 221, 927-937, 1994
 A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
 A:Reference number: S43545; PMID:94237157; PMID:8181475
 A:Content: annotation: conformation by (1)H-NMR, residues 96-184
 R:Rejante, M.; Llinas, M.
 Eur. J. Biochem. 221, 939-949, 1994
 A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
 A:Reference number: A58817; PMID:94237158; PMID:8181476
 A:Content: annotation: conformation by (1)H-NMR
 C:Comment: plasminogen is synthesized by the kidney and is present in plasma and many of
 C:Comment: plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU a
 d PIR:FGHUGB).
 C:Comment: plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITVUA2) immediately af
 rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor,
 C:Comment: Microplasmin is formed by autocatalytic cleavage of plasmin under artificial cond
 C:Comment: Streptolysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. Th
 ling solid tumors.
 C:Genetics:
 A:Gene: GDB:PLG
 A:Cross-references: GDB:119498; OMIM:173350
 A:Map position: 6q26-6q27
 A:Introns: 17/1; 62/2; 98/1, 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 528
 A:Function:
 C:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 n the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
 F:1-19/Domin: signal sequence #status predicted <SIG>
 F:20-810/Product: plasminogen #status predicted <PRO>
 F:20-96/Domin: activation peptide #status experimental <APT>
 F:79-466/Product: angiotensin #status experimental <AS>
 F:97-580,581-810/Product: plasmin #status experimental <AMT>
 F:97-580/Domin: plasmin chain A #status experimental <CHA>
 F:103-181/Domin: kringle homology <KR1>
 F:185-262/Domin: kringle homology <KR2>
 F:275-352/Domin: kringle homology <KR3>
 F:377-454/Domin: kringle homology <KR4>
 F:481-560/Domin: kringle homology <KR5>
 F:550-580,581-810/Product: microplasmin #status experimental <MPT>

Query Match 78.5%; Score 423; DB 1; Length 810;

Best Local Similarity 78.7%; Pred. No. 1e-33;
 Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 2 SPVQOCYCHGDDRSYVAGISSTVTGRTCCSWSMIPHHQORPENYPNAGLTENYCRND 61
 DB 371 TPVQOCYCHGDDQSRKGSITTTGKKCCSWSMIPHHQKTPENYPNAGLTENYCRND 430
 QY 62 SGKQPCYCTTDPCEVMEYCNLTQCSSETS 90
 DB 431 ADKGPCFTTDPSEVMEYCNLTQCSSETS 459
 RESULT 5
 PDBO
 Plasmin (EC 3.4.21.7) Precursor - bovine
 N/Alternate names: plasminogen
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 30-Sep-1987 #sequence, revision 28-Apr-1995 #text_change 18-Jun-1999
 C/Accession: S45046; A25835; I45961; S03736
 R/Berglund, L.; Andersen, M.D.; Petersen, T.E.
 submitted to the EMBL Data Library, May 1994
 A:Description: Cloning and characterization of the bovine plasminogen cDNA.
 A:Reference number: S45046
 A:Accession: S45046
 A:Molecule type: mRNA
 A:Residues: 1-812 <BER>
 A:Cross-references: EMBL:X79402; NID:G494962; PIDN:CAAS5939.1; PID:G494963
 A:Experimental source: Liver
 A/Note: It is uncertain whether Met-1 or Met-8 is the initiator
 R/Schaller, U.; Moser, P.W.; Danneberg-Muller, G.A.K.; Rosselet, S.J.; Kamfer, U.; Rick
 Eur. J. Biochem. 149, 267-278, 1985
 A:Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmi
 A:Reference number: A25835; PMID:85203906; PMID:3846532
 A:Accession: A25835
 A:Molecule type: protein
 A:Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
 R/Malnowski, D.P.; Sadler, J.E.; Davie, E.W.
 Biochemistry 23, 4243-4250, 1984
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and l
 A:Reference number: I45961; PMID:85023311; PMID:6148961
 A:Accession: I45961
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 706-743, 'R', 745-812 <MAL>
 A:Cross-references: GB:K02935; NID:G163551; PIDN:AAA0714.1; PID:G163552
 R/Brunsholz, R.A.; Lerch, P.G.; Schaller, U.; Rickli, E.E.; Legler, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human, l
 A:Reference number: S03735; PMID:81212097; PMID:7238497
 A:Accession: S03736
 A:Molecule type: protein
 A:Residues: 27-83

 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 n the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
 F:1-26/Domin: signal sequence #status predicted <SIG>
 F:8-103/Domin: plasminogen-related protein precursor homology <PLPH>
 F:27-103/Product: plasminogen #status experimental <PRO>
 F:27-103/Domin: activation peptide #status experimental <APT>
 F:104-583,584-812/Product: plasmin #status experimental <AMT>
 F:104-583/Domin: plasmin chain A #status experimental <ACH>
 F:110-188/Domin: kringle homology <KR1>
 F:192-269/Domin: kringle homology <KR2>
 F:282-359/Domin: kringle homology <KR3>
 F:384-461/Domin: kringle homology <KR4>
 F:485-564/Domin: kringle homology <KR5>
 F:584-812/Domin: plasmin chain B #status experimental <BCH>
 F:584-805/Domin: trypsin homology <TRY>
 F:56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,331
 bonds: #status predicted

A:Molecule type: protein
 A:Residues: 1-120 <SCH>
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: hydrolase; serine proteinase
 F:37-114/Domain: kringle homology <KR4>

Query Match 71.2%; Score 384; DB 2; Length 120;
 Best Local Similarity 70.9%; Pred. No. 1.1e-30;
 Matches 61; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 5 VDDCHGDRGSRYSSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 64
 DB 34 VDECHYQNGSGYSRGTSTTTGKRCQSSMTPHREKTPPEAGLTENYCRNP 93

QY 65 QPWCYTTPDCVRMEYCNLTQCSSETS 90
 DB 94 SPWCYTTPDSVRMEYCNLTQCSSETS 119

RESULT 12

146260 plasmin (EC 3.4.21.7) precursor - western European hedgehog
 C:Species: Erinaceus europaeus (western European hedgehog)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: 146260

R:Law, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995

A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein A:Reference number: 146259; MUID:96025778; PMID:7592597

A:Accession: 146260

A:Molecule type: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-810 <LAW>

A:Cross-references: EMBL:U33171, NID:g1046360, PID:g1046361

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: hydrolase; serine proteinase

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:379-456/Domain: kringle homology <KR4>

F:482-561/Domain: kringle homology <KR5>

F:582-803/Domain: trypsin homology <TRY>

Query Match 70.1%; Score 378; DB 2; Length 810;
 Best Local Similarity 68.5%; Pred. No. 2.6e-29;
 Matches 61; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 KSPVDDCHGDRGSRYSSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 60
 DB 372 QTPVDECTQNGSGYSRGTSTTTGKRCQSSMTPHREKTPPEAGLTENYCRNP 431

QY 61 DSGKQPCWCTTPDCVRMEYCNLTQCSSETS 89
 DB 432 DGDGKPCWCTTPDSVRMEYCNLTQCSSETS 460

RESULT 13

A40522 plasmin (EC 3.4.21.7) precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
 C:Accession: A40522

R:Kanalaab, U.J.; Makker, S.P.
 J. Biol. Chem. 266, 10825-10829, 1991

A:Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor

A:Reference number: A40522; MUID:91250378; PMID:1645711

A:Accession: A40522

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-169 <KAN>

A:Cross-references: GB:M62832; NID:g206215; PIDN:AAA1884.1; PID:g554488

A:Note: the authors translated the codon TCT for residue 76 as Ala

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:34-112/Domain: kringle homology <KR3>
 F:34-112,55-95,83-107/Disulfide bonds: #status predicted

Query Match 67.4%; Score 363.5; DB 2; Length 169;
 Best Local Similarity 65.2%; Pred. No. 1.5e-28;
 Matches 60; Conservative 15; Mismatches 16; Indels 1; Gaps 1;

QY 1 KSPVDDCHGDRGSRYSSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 60
 DB 27 QTPVDECTQNGSGYSRGTSTTTGKRCQSSMTPHREKTPPEAGLTENYCRNP 86

QY 61 DSGKQPCWCTTPDCVRMEYCNLTQCSSETS 91
 DB 87 DNDGKPCWCTTPDSVRMEYCNLTQCSSETS 118

RESULT 14

A60140 plasmin (EC 3.4.21.7) precursor - chicken (fragment)
 N:Alternate names: plasminogen
 C:Species: Gallus gallus (chicken)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
 C:Accession: A60140

R:Gyenes, M.; Pathy, L.
 Biochim. Biophys. Acta 832, 326-330, 1985

A:Title: The kringle 4 domain of chicken plasminogen.

A:Reference number: A60140; MUID:86077796; PMID:4074753

A:Accession: A60140

A:Molecule type: protein

A:Residues: 1-89 <GYE>

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase

F:6-83/Domain: kringle homology <KR3>
 F:6-83,27-66,55-78/Disulfide bonds: #status predicted

F:6-83/Binding site: carbonyl (Asn) (covalent) #status experimental

Query Match 61.0%; Score 329; DB 2; Length 89;
 Best Local Similarity 61.0%; Pred. No. 2e-25;
 Matches 50; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 6 ODCYGDGSRYSSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 65
 DB 4 EBCYQNGSVSRGTSTTTGKRCQSSMTPHREKTPPEAGLTENYCRNP 63

QY 66 PWCYTTPDCVRMEYCNLTQCSSETS 87
 DB 64 PWCYTTPDSVRMEYCNLTQCSSETS 85

RESULT 15

T18518 apolipoprotein(a) - western European hedgehog (fragment)
 C:Species: Erinaceus europaeus (western European hedgehog)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
 C:Accession: T18518

R:Law, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995

A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein A:Reference number: T18518; MUID:96025778; PMID:7592597

A:Accession: T18518

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2869 <LAW>

A:Cross-references: EMBL:U33170, NID:g1046358; PID:g1046359; PIDN:AA40522.1

A:Experimental source: liver

C:Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con-

tent apolipoprotein(a).

Query Match 52.1%; Score 281; DB 2; Length 2869;
 Best Local Similarity 51.7%; Pred. No. 2.7e-19;
 Matches 45; Conservative 8; Mismatches 34; Indels 0; Gaps 0;

Qy 4 VVODCYHGDGRSYRGTSSTVTGRTCOSWGSWI PHWQRTTPENYPNAGLTENYCRNPDG 63
Db 2680 IPDQCLEGTGENTRGSAVATVSGHTCORMRQSBHSHSRTPENYPTNLFQNYCRNPDGE 2739
Qy 64 KOPWCYTTDPQVWMEYCNLTQCSSETS 90
Db 2740 VAPWCYTTNSAVRMEYCKIPSCNSSS 2766

Search completed: January 12, 2004, 17:26:23
Job time : 12.3158 secs

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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:17:22 ; Search time 7.86842 Seconds

(without alignments)
543.874 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539

Sequence: 1 KSPVQDCHGDDGRSYRGIS.....DPCVMEXCNLTQCESETESG 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 41.1*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	539	100.0	4548	1	APOA_HUMAN
2	515	95.5	1420	1	APOA_MACMU
3	425	78.8	810	1	PLMN_MACMU
4	423	78.5	810	1	PLMN_HUMAN
5	413	76.6	812	1	PLMN_BOVIN
6	402	74.6	790	1	PLMN_PIG
7	388	72.0	812	1	PLMN_MOUSE
8	378	70.1	810	1	PLMN_ERIEU
9	363.5	67.4	169	1	HGF_HUMAN
10	255	47.3	728	1	HGF_HUMAN
11	250	46.4	728	1	HGF_RAT
12	249	46.2	728	1	HGF_MOUSE
13	241.5	44.8	716	1	HGFL_MOUSE
14	236	43.8	343	1	PLMN_SHEEP
15	231.5	42.9	711	1	HGFL_HUMAN
16	226	41.9	333	1	PLMN_CANPA
17	222	41.2	338	1	PLMN_HORSE
18	204	37.8	325	1	PLMN_PETMA
19	201.5	37.4	622	1	THRB_HUMAN
20	200.5	37.2	943	1	ROR2_HUMAN
21	200	37.1	617	1	THRB_RAT
22	196	36.4	618	1	THRB_MOUSE
23	195.5	36.3	944	1	ROR2_MOUSE
24	193.5	35.9	625	1	THRB_BOVIN
25	193.5	35.9	724	1	ROR2_DROME
26	190.5	35.3	937	1	ROR1_MOUSE
27	189.5	35.2	937	1	ROR1_HUMAN
28	186	34.5	562	1	TPA_HUMAN
29	181.5	33.7	603	1	FAI2_CAVPO
30	181.5	33.7	615	1	FAI2_HUMAN
31	177	32.8	565	1	TPA_BOVIN
32	177	32.8	559	1	HGFA_MOUSE
33	176.5	32.7	559	1	TPA_RAT

34	173.5	32.2	593	1	FAI2_BOVIN	P98140 bos taurus
35	173	32.1	655	1	HGFA_HUMAN	Q04756 homo sapien
36	172	31.9	559	1	TPA_MOUSE	P11214 mus musculus
37	166	30.8	432	1	UROK_RAT	P29598 rattus norv
38	163	30.2	462	1	KRM2_HUMAN	O88cwo homo sapien
39	161.5	30.0	473	1	KRM1_MOUSE	Q99n43 mus musculus
40	161.5	30.0	473	1	UROK_PIG	Q92484 rattus norv
41	161	29.9	442	1	UROK_PIG	P04185 sus scrofa
42	158.5	29.4	475	1	KRM1_HUMAN	Q96m88 homo sapien
43	158	29.3	461	1	KRM2_MOUSE	O8k187 mus musculus
44	157.5	29.2	452	1	KRM1_XENTLA	Q90y90 xenopus lae
45	157	29.1	433	1	UROK_MOUSE	P06869 mus musculus

ALIGNMENTS

RESULT 1
ID APOA_HUMAN STANDARD; PRT; 4548 AA.
AC P08519;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
GN LPA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=88039109; PubMed=3570400;
RA McLean J.M., Tomlinson J.E., Kang W.-J., Eaton D.L., Chen E.Y.,
RT Fless G.M., Scann A.M., Lawn R.M.;
RT "CDNA sequence of human apolipoprotein(a) is homologous to
RT plasminogen.";
RL Nature 330:132-137(1987).
RN [2]
RP SERINE PROTEASE ACTIVITY.
RX MEDLINE=90076123; PubMed=2531657;
RA Salonen E.-M., Jauhainen M., Zardi L., Vaheri A., Ehnholm C.;
RT "Lipoprotein(a) binds to fibronectin and has serine proteinase
RT activity capable of cleaving it.";
RL EMBO J. 8:4035-4040(1989).
RN [3]
RP REVIEW.
RX MEDLINE=90049223; PubMed=2530631;
RA Utermann G.;
RT "The mysteries of lipoprotein(a)." ;
RL Science 246:904-910(1989).
RN [4]
RP CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
RX MEDLINE=21303595; PubMed=11294842;
RA Garner B., Merry A.H., Royle L., Harvey D.U., Rudd P.M., Thillet J.;
RT "Structural elucidation of the N- and O-glycans in conferring protease
RT apolipoprotein(a): role of o-glycans in conferring protease
RT resistance." ;
RL J. Biol. Chem. 276:22200-22208(2001).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
RX MEDLINE=96217891; PubMed=8642595;
RA Mikol V., Lograsso P.V., Boettcher B.R.;
RT "Crystal structures of apolipoprotein(a) kringle IV37 free and
RT complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
RT acid: existence of novel and expected binding modes." ;
RL J. Mol. Biol. 256:751-761(1996).
RN [6]
RP VARIANT ARG-4193.
RX MEDLINE=95002201; PubMed=7918682;
RA Scann A.M., Pfaffinger D., Lee J.C., Himman J.;
RT "A single point mutation (Trp72->Arg) in human apo(a) kringle 4-37
RT associated with a lysine binding defect in Lp(a)." ;

RL Blochim. Biophys. Acta 1227:41-45(1994).
 CC -1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
 CC (Lp(a)). It has serine proteinase activity and is able of
 CC autoproteolysis. Inhibits tissue-type plasminogen activator 1.
 CC Lp(a) may be a ligand for megalin/Gp 330.
 CC -1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibrinectin and
 CC decorin.
 CC -1- PTM: N- and O-glycosylated. The N-glycans are complex biantennary
 CC structures present in either a mono- or disialylated state. The
 CC O-glycans are mostly (80%) represented by the monosialylated core
 CC type I structure, NeuNAc2Galbeta1-3GalNAc, with smaller
 CC amounts of disialylated and non-sialylated O-glycans also
 CC detected.
 CC -1- DISEASE: Elevated plasma concentrations of apo(a) and its
 CC naturally occurring proteolytic fragments are correlated with
 CC atherosclerosis. Homology with plasminogen kringle IV and V is
 CC thought to underlie the atherogenicity of the protein, because the
 CC fragments are competing with plasminogen for fibrinogen binding.
 CC -1- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
 CC leading to the formation of the so called mini-Lp(a). Apo(a)
 CC fragments accumulate in atherosclerotic lesions, where they may
 CC promote thrombogenesis. O-glycosylation may limit the extent of
 CC proteolytic fragmentation.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 38 kringle domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X06290; CAA29618.1; -.
 CC PIR: S00657; S00657.
 CC PDB: 1I71; 13-JUN-01.
 CC PDB: 1JFN; 28-JUN-02.
 CC PDB: 1KIV; 18-MAY-99.
 CC PDB: 3KIV; 18-MAY-99.
 CC PDB: 4KIV; 18-MAY-99.
 CC MEROPS: S01.226; -.
 CC GeneW: HGNC:6667; LPA.
 CC MIM: 152200; -.
 CC GO: GO:000466; F: endopeptidase inhibitor activity; TAS.
 CC GO: GO:0008015; P: circulation; TAS.
 CC GO: GO:0009405; P: pathogenesis; TAS.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR001254; Ser protease_Try.
 CC Pfam: PF00051; kringle_38.
 CC Pfam: PF00089; trypsin_1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00018; KRINGLE.
 CC ProDom: PD000395; Kringle_38.
 CC SMART: SM00130; KR_38.
 CC SMART: SM00020; TRYPTIC_1.
 CC PROSITE: PS00021; KRINGLE_1; 38.
 CC PROSITE: PS00070; KRINGLE_2; 38.
 CC PROSITE: PS00240; TRYPSIN_DOM_1.
 CC PROSITE: PS00134; TRYPSIN_HIS_1.
 CC PROSITE: PS00135; TRYPSIN_SER_1.
 CC HydroLase: Serine protease; Lipid transport; Plasma; Glycoprotein;
 CC Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.
 CC KW HydroLase; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.
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 CC KRINGLE

RL J. Biol. Chem. 264:5957-5965(1989).
 CC -1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
 CC (Lp(a)). It has serine proteinase activity and is able of
 CC autolysis. Inhibits tissue-type plasminogen activator 1.
 CC Lp(a) may be a ligand for megalin/Gp 330.
 CC -1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
 CC decorin (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- DISASE: Elevated plasma concentrations of apo(a) and its
 CC naturally occurring proteolytic fragments are correlated with
 CC atherosclerosis. Homology with plasminogen kringle IV and V is
 CC thought to underlie the atherogenicity of the protein, because the
 CC fragments are competing with plasminogen for fibrin(ogen) binding.
 CC MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
 CC leading to the formation of the so called mini-Lp(a). Apo(a)
 CC fragments accumulate in atherosclerotic lesions, where they may
 CC promote thrombogenesis. O-glycosylation may limit the extent of
 CC proteolytic fragmentation (By similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains at least 10 kringle domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, J04635; AAA36833.1; -.
 CC DR PIR: A32869; A32869.
 CC DR HSP: P00747; 2PK4.
 CC DR MEROPS: S01.226;
 CC DR InterPro: IPR001314; Chymotrypsin.
 CC DR InterPro: IPR000001; Kringle.
 CC DR InterPro: IPR001254; Ser. protease_Try.
 CC DR Pfam: PF00051; kringle; 11.
 CC DR Pfam: PF00089; trypsin; 1.
 CC DR PRINTS: PR00722; CHYMOTRYPSIN.
 CC DR PRINTS: PR00018; KRINGLE.
 CC DR ProDom: PD000395; kringle; 10.
 CC DR SMART: SM00130; KR; 10.
 CC DR SMART: SM00020; Tcyp_Spc; 1.
 CC DR PROSITE: PS00021; KRINGLE_1; 10.
 CC DR PROSITE: PS0070; KRINGLE_2; 10.
 CC DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 CC DR PROSITE: PS00134; TRYPSIN_HIS; FALSE NEG.
 CC DR PROSITE: PS00135; TRYPSIN_SER; FALSE NEG.
 CC DR Hydrolase: Serine protease; Lipid transport; Plasma; Glycoprotein;
 CC Kringle; Repeat; Atherosclerosis.
 CC KM Kringle; Repeat; Atherosclerosis.
 CC FT NON_TER 1 1
 CC FT DOMAIN 49 127 KRINGLE 1.
 CC FT DOMAIN 163 241 KRINGLE 2.
 CC FT DOMAIN 277 355 KRINGLE 3.
 CC FT DOMAIN 391 469 KRINGLE 4.
 CC FT DOMAIN 505 583 KRINGLE 5.
 CC FT DOMAIN 619 697 KRINGLE 6.
 CC FT DOMAIN 725 803 KRINGLE 7.
 CC FT DOMAIN 839 917 KRINGLE 8.
 CC FT DOMAIN 953 1031 KRINGLE 9.
 CC FT DOMAIN 1067 1145 KRINGLE 10.
 CC FT DOMAIN 1191 1420 KRINGLE 10.
 CC FT SEQUENCE 1420 AA; 158367 MW; BE102949E0305B0E CRC64;
 CC
 CC Query Match 95.5%; Score 515; DB 1; Length 1420;
 CC Best Local Similarity 94.5%; Pred. No. 1.7e-45;
 CC Matches 86; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KSPVVDCTCHGGRSRTGISSTTVTKTQSSNTPPHMHQTPPEYPAAGLTENYCNRP 60
 DB 947 KSPVVDCTCHGGRSRTGISSTTVTKTQSSNTPPHMHQTPPEYPAAGLTENYCNRP 1006
 QY 61 DSGKPCWCTTDPICVMEYCNLTQCSFTSG 91

DB 1007 DSGKPCWCTTDPICVMEYCNLTQCSFTSG 1037
 |||||
 RESULT 3
 ID PLNM MACMU STANDARD; PRT; 810 AA.
 AC PLNM MACMU
 ID 12545;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen precursor (BC 3.4.21.7).
 GN FIG.
 OS Maccaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butcheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89174660; PubMed=2925643;
 RA Tomlinson J.E., McLean J.W., Lawn R.M.;
 RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 RT synthesis.";
 RL J. Biol. Chem. 264:5957-5965(1989).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UKONINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD
 CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, J04697; AAA36901.1; -.
 CC DR PIR: B32869; B30848.
 CC DR HSP: P00747; 1PMK.
 CC DR MEROPS: S01.233; -.
 CC DR InterPro: IPR001314; Chymotrypsin.
 CC DR InterPro: IPR000001; Kringle.
 CC DR InterPro: IPR003014; PAN.
 CC DR InterPro: IPR003609; Pan_app.
 CC DR InterPro: IPR003966; Prothrombin.
 CC DR InterPro: IPR001254; Ser. protease_Try.
 CC DR Pfam: PF00051; kringle; 5.
 CC DR Pfam: PF00024; PAN; 1.
 CC DR Pfam: PF00089; trypsin; 1.
 CC DR PRINTS: PR00722; CHYMOTRYPSIN.
 CC DR PRINTS: PR00018; KRINGLE.
 CC DR PRINTS: PR01505; PROTHROMBIN.
 CC DR ProDom: PD000395; Kringle; 5.


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DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; TYP SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS50070; KRINGLE_2; 5.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Hydroxase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL. 1 19
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 184 262 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 377 454 KRINGLE 4.
FT DOMAIN 481 560 KRINGLE 5.
FT DOMAIN 581 810 SERINE PROTEASE.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT ACT_SITE 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 158 158 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 432 432 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 134 134 FIBRIN.
FT BINDING 136 136 FIBRIN.
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 61 BY SIMILARITY.
FT DISULFID 103 181 BY SIMILARITY.
FT DISULFID 124 164 BY SIMILARITY.
FT DISULFID 152 176 BY SIMILARITY.
FT DISULFID 185 262 BY SIMILARITY.
FT DISULFID 188 316 BY SIMILARITY.
FT DISULFID 206 245 BY SIMILARITY.
FT DISULFID 234 257 BY SIMILARITY.
FT DISULFID 275 352 BY SIMILARITY.
FT DISULFID 296 335 BY SIMILARITY.
FT DISULFID 324 347 BY SIMILARITY.
FT DISULFID 377 454 BY SIMILARITY.
FT DISULFID 398 437 BY SIMILARITY.
FT DISULFID 426 449 BY SIMILARITY.
FT DISULFID 481 560 BY SIMILARITY.
FT DISULFID 502 543 BY SIMILARITY.
FT DISULFID 531 555 BY SIMILARITY.
FT DISULFID 567 685 BY SIMILARITY.
FT DISULFID 577 585 BY SIMILARITY.
FT DISULFID 607 623 BY SIMILARITY.
FT DISULFID 699 766 BY SIMILARITY.
FT DISULFID 729 745 BY SIMILARITY.
FT DISULFID 756 784 BY SIMILARITY.
FT CARBOHYD 365 365 O-LINKED (GALNAAC...) (BY SIMILARITY).
SQ SEQUENCE 810 AA; 90255 MW; A7SEIC51A1A0F24A CRC64;

Query Match 78.8%; Score 425; DB 1; Length 810;
Best Local Similarity 77.3%; Pred. No. 1.9e-36;
Matches 68; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

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RESULT 4
PLAN HUMAN
ID PLAN HUMAN STANDARD; PRT; 810 AA.
AC P00747;
DT 21-UTL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
GN PLG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90202879; PubMed=2318848;
RA Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;
RT "Characterization of the gene for human plasminogen, a key proenzyme
in the fibrinolytic system."
RL J. Biol. Chem. 265:6104-6111 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87162490; PubMed=3030813;
RA Forsgren M., Raden B., Ibraheemson M., Larsson K., Heden L.-O.;
RT "Molecular cloning and characterization of a full-length cDNA clone
for human plasminogen."
RL FEBS Lett. 213:254-260 (1987).
RN [3]
RP SEQUENCE OF 20-810.
RA Sottrup-Jensen L., Petersen T.E., Magnusson S.;
RT Submitted (JUL-1977) to the PIR data bank.
RN [4]
RP SEQUENCE OF 292-810 FROM N.A.
RX MEDLINE=85023311; PubMed=6148961;
RA Malinowski D.P., Sadler J.E., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
human and bovine plasminogen."
RL Biochemistry 23:4243-4250 (1984).
RN [5]
RP SEQUENCE OF 20-100.
RX MEDLINE=75093329; PubMed=122932;
RA Wiman B., Wallen P.;
RT "Structural relationship between 'glutamic acid' and 'lysine' forms
of human plasminogen and their interaction with the NH2-terminal
activation peptide as studied by affinity chromatography."
RL Eur. J. Biochem. 50:489-494 (1975).
RN [6]
RP SEQUENCE OF 95-580, 581-626; 657-700 AND 732-810.
RA Sottrup-Jensen L., Claess H., Zajdel M., Petersen T.E., Magnusson S.;
RT (in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);
Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
Raven Press, New York (1978).
RN [7]
RP SEQUENCE OF 483-604.
RX MEDLINE=76043692; PubMed=126863;
RA Wiman B., Wallen P.;
RT "Amino-acid sequence of the cyanogen-bromide fragment from human
plasminogen that forms the linkage between the plasmin chains."
RL Eur. J. Biochem. 58:539-547 (1975).
RN [8]
RP SEQUENCE OF 581-810.
RX MEDLINE=77225245; PubMed=142009;
RA Wiman B.;
RT "Primary structure of the B-chain of human plasmin."
RL Eur. J. Biochem. 76:129-137 (1977).
RN [9]
RP ACTIVE SITE.
RX MEDLINE=73149248; PubMed=4694729;
RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
RT "The primary structure of human plasminogen. II. The histidine loop
of human plasmin: light (B) chain active center histidine sequence."
RL J. Biol. Chem. 248:1631-1633 (1973).
RN [10]

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RP ACTIVE SITE.
 RX MEDLINE=69234739; Pubmed=4240117;
 RA Groshopf W.R., Sumaria L., Robbins K.C.;
 RT "Studies on the active center of human plasmin. Partial amino acid
 RT sequence of a peptide containing the active center serine residue.";
 RL J. Biol. Chem. 244:3590-3597(1969).
 RN [11]
 RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
 RX MEDLINE=82213905; Pubmed=6919539;
 RA Trexler M., Vaili Z., Patchy L.;
 RT "Structure of the omega-aminocarbonylic acid-binding sites of human
 RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
 RT binding of ligand by kringle 4.";
 RL J. Biol. Chem. 257:7401-7406(1982).
 RN [12]
 RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
 RX MEDLINE=8054794; Pubmed=6094526;
 RA Vaili Z., Patchy L.;
 RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
 RT are essential for fibrin affinity of the kringle 1 domain.";
 RL J. Biol. Chem. 259:13690-13694(1984).
 RN [13]
 RP PHOSPHORYLATION SITE SER-597
 RX MEDLINE=97345939; Pubmed=9201958;
 RA Wang H., Proctor M., Bretthauer R.K., Castellino F.J.;
 RT "Serine-578 is a major phosphorylation locus in human plasma
 RT plasminogen.";
 RL Biochemistry 36:8100-8106(1997).
 RN [14]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; Pubmed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RT Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 RN [15]
 RP CARBOHYDRATE-LINKAGE SITE SER-268.
 RX MEDLINE=97207306; Pubmed=9054441;
 RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Englund J.J.,
 RA Pizzo S.V.;
 RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
 RT human plasminogen 2.";
 RL J. Biol. Chem. 272:7408-7411(1997).
 RN [16]
 RP CHARACTERIZATION OF ANGIOSTATIN AND PARTIAL SEQUENCE.
 RX MEDLINE=95042728; Pubmed=7525077;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 RT suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328(1994).
 RN [17]
 RP CHARACTERIZATION OF ANGIOSTATIN.
 RX MEDLINE=97238710; Pubmed=9102221;
 RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
 RA Lapevich R., Nacy C.A.;
 RT "A recombinant human angiostatin protein inhibits experimental primary
 RT and metastatic cancer.";
 RL Cancer Res. 57:1329-1334(1997).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
 RX MEDLINE=92031502; Pubmed=1657146;
 RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
 RT "Crystal and molecular structure of human plasminogen kringle 4
 RT refined at 1.9-A resolution.";
 RL Biochemistry 30:10576-10588(1991).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
 RX MEDLINE=92031503; Pubmed=1657149;
 RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
 RT "The refined structure of the epsilon-aminocaproic acid complex of

RT human plasminogen kringle 4.";
 RL Biochemistry 30:10589-10594(1991).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
 RA Stec B., Yamano A., Whitlow M., Teeter M.M.;
 RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
 RT A possible structural role of disordered residues.";
 RL Acta Crystallogr. D 53:169-178(1997).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
 RX MEDLINE=96180681; Pubmed=8611560;
 RA Mathews I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.;
 RT "Crystal structures of the recombinant kringle 1 domain of human
 RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
 RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic Acid.";
 RL Biochemistry 35:2567-2576(1996).
 RN [22]
 RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
 RX MEDLINE=98198034; Pubmed=9521645;
 RA Chang Y., Mochalkin I., Mccance S.G., Cheng B., Tulinsky A.,
 RA Castellino F.J.;
 RT "Structure and ligand binding determinants of the recombinant kringle
 RT 5 domain of human plasminogen.";
 RL Biochemistry 37:3258-3271(1998).
 RN [23]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237157; Pubmed=8181475;
 RA Rejante M.R., Llinas M.;
 RT "1H-NMR assignments and secondary structure of human plasminogen
 RT kringle 1.";
 RL Eur. J. Biochem. 221:927-937(1994).
 RN [24]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237158; Pubmed=8181476;
 RA Rejante M.R., Llinas M.;
 RT "Solution structure of the epsilon-aminohexanoic acid complex of
 RT human plasminogen kringle 1.";
 RL Eur. J. Biochem. 221:939-949(1994).
 RN [25]
 RP STRUCTURE BY NMR OF 183-354.
 RX MEDLINE=96194156; Pubmed=8652577;
 RA Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
 RA Rickli E.E.;
 RT "Recombinant gene expression and 1H NMR characteristics of the
 RT kringle (2 + 3) supermodule; spectroscopic/functional individuality
 RT of plasminogen kringle domains.";
 RL Biochemistry 35:2357-2364(1996).
 RN [26]
 RP STRUCTURE BY NMR OF 374-461.
 RX MEDLINE=90219023; Pubmed=2157950;
 RA Atkinson R.A., Williams R.J.P.;
 RT "Solution structure of the kringle 4 domain from human plasminogen by
 RT 1H nuclear magnetic resonance spectroscopy and distance geometry.";
 RL J. Mol. Biol. 212:541-552(1990).
 RN [27]
 RP VARIANTS PHE-374 AND THR-620.
 Query Match 78.5%; Score 423; DB 1; Length 810;
 Best Local Similarity 78.7%; Pred. No. 3; 1e-36;
 Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 2 SPVDDCHGDSRGISSTVTGRTQSWSMIPHHORTPEYVPAAGLTENYCRPD 61
 DB 371 TPVDDCHGDSRGISSTVTGRTQSWSMTPHHOKTPEYVPAAGLTENYCRPD 430
 QY 62 SCKQPCWCTTDCVWEXCNLTQCSSETS 90
 DB 431 ADKGPWCFTTDBSVWBYCNLKKSGTEA 459
 RESULT 5
 PLNR BOVIN
 ID PLNR_BOVIN STANDARD; PRT; 812 AA.

AC P06868; Q28162; (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 41, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7).
 GN PIG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_taxid=9913;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Berglund L., Andersen M.D., Petersen T.E.;
 RT "Cloning and characterization of the bovine plasminogen cDNA";
 RL Int. Dairy J. 5:593-603(1995).
 RN [2]
 RP SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=85203906; PubMed=3846532;
 RA Schaller J., Moser P.W., Danneberg-Muller G.A.K., Rosset S.J.,
 RA Kamper U., Rickli E.E.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with
 RT human plasminogen."; Biochem. 149:267-278(1985).
 RL Eur. J. Biochem. 149:267-278(1985).
 RN [3]
 RP SEQUENCE OF 706-812 FROM N.A.
 RX MEDLINE=85023311; PubMed=6148961;
 RA Mallinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT human and bovine plasminogen."; Biochemistry 23:4243-4250(1984).
 RL Biochemistry 23:4243-4250(1984).
 RN [4]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamberling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns."; Eur. J. Biochem. 173:57-63(1988).
 RL Eur. J. Biochem. 173:57-63(1988).
 RN [5]
 RP FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC PPM: N-LINKED GLYCAN CONTAIN N-ACETYLACTOSAMINE AND SIALIC ACID.
 CC O-LINKED GLYCANS CONSIST OF GAL-GALNAc DISACCHARIDE WITH IS
 CC MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
 CC MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC SIMILARITY: Contains 5 kringle domains.
 CC -----
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 CC -----
 CC DR EMBL; X79402; CAAS5939.1; -;
 CC EMBL; K02935; AAA30714.1; -;

DR PIR; S45046; PLBO.
 DR HSSP; P00747; 2PK4.
 DR MEROPS; S01.233; -;
 DR GlycoSuiteDB; P06868; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser protease_Try.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS50070; KRINGLE_2; 5.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Serine protease; Plasma; glycoprotein; Fibrinolysis;
 KM Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KM Signal.
 FT SIGNAL. 1 26
 FT CHAIN 27 812 PLASMINOGEN.
 FT CHAIN 27 583 PLASMIN HEAVY CHAIN A.
 FT CHAIN 584 812 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 110 188 KRINGLE 1.
 FT DOMAIN 192 269 KRINGLE 2.
 FT DOMAIN 282 359 KRINGLE 3.
 FT DOMAIN 384 461 KRINGLE 4.
 FT DOMAIN 485 564 KRINGLE 5.
 FT DOMAIN 584 812 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 315 315 O-LINKED (GALNAc. . .).
 FT CARBOHYD 365 365 /FTID-CAR 000015.
 FT ACT_SITE 624 624 CHARGE RELAY SYSTEM.
 FT ACT_SITE 667 667 CHARGE RELAY SYSTEM.
 FT ACT_SITE 762 762 CHARGE RELAY SYSTEM.
 FT CONFLICT 335 335 N -> D (IN REF. 2).
 FT CONFLICT 516 516 O -> H (IN REF. 2).
 FT CONFLICT 555 555 P -> L (IN REF. 2).
 FT CONFLICT 744 744 T -> R (IN REF. 3).
 SQ SEQUENCE 812 AA; 91216 MW; 38A6A691E20946 CRC64;
 Query Match 76.6%; Score 413; DB 1; Length 812;
 Match Local Similarity 77.3%; Pred. No. 3,3e-35;
 Matches 68; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 KSPVVDCHYGDRSYRGISSTVTGRTGQSSWMIPIHWHORTPENYPNAGLTENYCRNP 60
 DB 377 QTVPPDCYHGNGSYRGISSTVTITRKCKQSWSPHRLTKTPENYPNAGLTMYNCRNP 436
 QY 61 DSGKQPCWCTTTPDCYAWCYCNLTQCSST 88
 DB 437 DADKSPWCYTTPDPRVMEPCNLKCKSET 464
 RESULT 6
 PLMN_PIG ID PLMN_PIG STANDARD; PRT; 790 AA.
 AC P06867;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen (EC 3.4.21.7).
 GN PIG.

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulky S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Maan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rutterfield Y.S.N., Krzywnski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903(2002).
RL *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1-16 FROM N.A.
RC STRAIN-129/STJ; TISSUE=Liver;
RX PubMed=12149246;
RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA Palmer R.J., Miles L.A.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma." *Cell* 79:315-328(1994).
RL *Cell* 79:315-328(1994).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION. IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
CC NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
CC METASTATIC TUMORS IN VIVO.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STEPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
CC INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kirtle domains.

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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; J04766; AAA50168.1; -;
DR EMBL; AF481053; AAM22156.1; -;
DR EMBL; BC014773; AAH14773.1; -;
DR EMBL; AY134430; AAN15805.1; -;
DR PIR; A38514; PLMK.
DR HSSP; P00747; IPMK.
DR MEROPS; S01.233; -;
DR MGD; MGI:97620; Plg.
DR GO; GO:0016506; F:apoptosis activator activity; IDA.
DR GO; GO:0006915; F:apoptosis; IDA.
DR InterPro; IPR001314; Chymotrypsin.

[illegible]

Query Match	72.0%;	Score 388;	DB 1;	Length 812;
Best Local Similarity	70.5%;	Pred. No. 1.3e-32;		
Matches 62;	Conservative 12;	Mismatches 14;	Indels 0;	Gaps 0
QY	1	KSPVQDCIHDGDSYRGISSTVTYGTGCQSMSSMIPHHQRTPEPNYDPAIGLTENYCANP	60	

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Db      370 QTPVVECYGQSDQSYRGTSSTITGKKCSMAAMPHRHRSKTEPNFPAGLEMYCNP 429
QY      61 DSGKQPMCTTDPCCVMEYCNLTQCSSE 88
Db      430 DSGKQPMCTTDPCCVMEYCNLTQCSSE 457

RESULT 8
PLMN_ERIEU STANDARD; PRT; 810 AA.
ID PLMN_ERIEU STANDARD; PRT; 810 AA.
AC Q29485;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
PLG.
Etrinaeus europaeus (Western European hedgehog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
NCBI_TaxId=9365;
[1]
SEQUENCE FROM N.A.
TISSEUE=Liver;
MEDLINE=96025778; PubMed=7592597;
Lawn R.M., Boommark N.W., Schwartz K., Lindahl G.B., Wade D.P.,
Byrne C.D., Fong K.J., Meer K., Patchy L.,
"the recurring evolution of lipoprotein(a). Insights from cloning of
hedgehog apolipoprotein(a).";
J. Biol. Chem. 270:24004-24009(1995).
[2]
REVISIONS.
Lawn R.M.;
Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
-|- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE
GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
LAMININ AND VON WILLEBRAND FACTOR.
-|- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
higher selectivity than trypsin. Converts fibrin into soluble
products.
-|- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
-|- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
-|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
-|- SIMILARITY: Contains 5 kringles domains.
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DR EMBL, U31171; AAC48717.1; -
DR PIR, I46260; I46260.
DR HSP, P00747; 1PMK.
DR MEROPS, S01.233; -
DR InterPro, IPR001314; Chymotrypsin.
DR InterPro, IPR000001; Kringles.
DR InterPro, IPR003014; PAN.
DR InterPro, IPR003609; Pan_app.
DR InterPro, IPR003966; Prothrombin.
DR InterPro, IPR001254; Ser_protease_Try.
DR Pfam, PF00051; kringles; 5.
DR Pfam, PF00024; PAN; 1.

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DR Pfam, PF00089; trypsin; 1.
DR PRINTS, PR00722; CHYMOTRYPSIN.
DR PRINTS, PR00018; KRINGLE.
DR PRINTS, PR01505; PROTHROMBIN.
DR ProDom, PD000395; Kringles; 5.
DR SMART, SM00130; KR; 5.
DR SMART, SM00473; PAN_AP; 1.
DR SMART, SM00020; TRYD_SPE; 1.
DR PROSITE, PS00020; KRINGLE_1; 5.
DR PROSITE, PS00070; KRINGLE_2; 5.
DR PROSITE, PS00240; TRYPSIN_DOM; 1.
DR PROSITE, PS00134; TRYPSIN_HIS; 1.
DR PROSITE, PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
Tissue remodeling; Blood coagulation; Kringles; Zymogen; Repeat;
KW Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
FT DOMAIN 583 810 SERINE PROTEASE.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 185 262 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 379 456 KRINGLE 4.
FT DOMAIN 482 561 KRINGLE 5.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT CARBOHYD 339 339 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 810 AA; 90902 MW; 8E5780946017A16 CRC64;

Query Match 70.1%; Score 378; DB 1; Length 810;
Best Local Similarity 68.5%; Pred. No. 1,4e-31;
Matches 61; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 KSPVQDCEYHGDGSRYSSTTVYGRTCQSSMI PPHORTPEYNPAGLTENYCNP 60
DB 372 QTPVVECYGQSDQSYRGTSSTITGKKCSMAAMPHRHRSKTEPNFPAGLEMYCNP 431
QY 61 DSGKQPMCTTDPCCVMEYCNLTQCSSE 89
DB 432 DSGKQPMCTTDPCCVMEYCNLTQCSSE 460

RESULT 9
PLMN_RAT STANDARD; PRT; 169 AA.
ID PLMN_RAT STANDARD; PRT; 169 AA.
AC Q01177;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
PLG.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxId=10116;
[1]
SEQUENCE FROM N.A.
TISSEUE=Liver;
MEDLINE=91250379; PubMed=1645711;
Kanalas U.J., Makker S.P.,
"Identification of the rat Heymann nephritis autoantigen (GP330) as a
receptor site for plasminogen.";
J. Biol. Chem. 266:10825-10829(1991).
-|- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE
GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,

```

CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringle domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M62832; AAA1884.1; -.
CC PIR: A40522; A40522.
CC HSSP: P00747; 1PMK.
CC MEROPS: S01.233; -.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR003966; Prothrombin.
CC InterPro: IPR001254; Ser. protease_Try.
CC Pfam: PF00051; Kringle; 2.
CC PRINTS: PR00018; KRINGLE.
CC PRINTS: PR01505; PROTHROMBIN.
CC ProDom: PD000395; Kringle; 2.
CC SMART: SM00130; KR_1.
CC PROSITE: PS00021; KRINGLE_1; 1.
CC PROSITE: PS50070; KRINGLE_2; 2.
CC PROSITE: PS50240; TRYPSIN_DOM; PARTIAL.
CC PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
CC PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
CC HydroLase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
CC Tissue remodeling; Blood coagulation; Kringle; Repeat.
CC KM NON_TER 1 1
CC FT DOMAIN 1 1
CC FT DOMAIN 34 112 KRINGLE 3 (BY SIMILARITY).
CC FT DOMAIN 139 >169 KRINGLE 4 (BY SIMILARITY).
CC FT DISULFID 34 112 KRINGLE 5 (BY SIMILARITY).
CC FT DISULFID 55 95 BY SIMILARITY.
CC FT DISULFID 83 107 BY SIMILARITY.
CC FT NON_TER 169 169
CC SQ SEQUENCE 169 AA; 18401 MW; 77A54214C49D010C CRC64;
Query Match 67.4%; Score 363.5; DB 1; Length 169;
Best Local Similarity 65.2%; Pred. No. 8.5e-31;
Matches 60; Conservative 15; Mismatches 16; Indels 1; Gaps 1;
Qy 1 KSPVQDCYAGDGRSGYRISSTVYTGRTCSWSSMIPHMQRPPENYNNAGLTENYCRNP 60
Db 27 QTEPVQDCYAGDGRSGYRISSTVYTGRTCSWSSMIPHMQRPPENYNNAGLTENYCRNP 86
Qy 61 DSGKQ-PWCYTTTDPCTWMEYCNLTQCSSTSG 91
Db 87 DNDQRGPCWCTTDPSPVMEYCNLTQCSSTSG 118
RESULT 10
HGF_HUMAN STANDARD; PRT; 728 AA.
ID HGF_HUMAN
AC P14210; Q9BYL9; Q9UDU6;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoietin A).
GN HGF OR HPTA.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91340155; PubMed=1831432;
RA Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
RT "Organization of the human hepatocyte growth factor-encoding gene.";
RL Gene 102:213-219(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91340155; PubMed=2528952;
RA Miyazawa K., Teubouchi H., Naka D., Takahashi K., Okiyaki M.,
RA Arakaki N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,
RA Gohda E., Daikuhara Y., Kitamura N.;
RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
RT growth factor.";
RL Biochem. Biophys. Res. Commun. 163:967-973(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Leukocyte;
RC MEDLINE=91025062; PubMed=2145836;
RA Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T.,
RA Asahi O., Hagiya M., Nakamura T., Shimizu S.;
RT "Isolation and expression of cDNA for different forms of hepatocyte
RT growth factor from human leukocyte.";
RL Biochem. Biophys. Res. Commun. 172:321-327(1990).
RN [4]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 55-73 AND 495-520.
RX TISSUE=Liver;
RC MEDLINE=90066676; PubMed=2531289;
RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,
RA Sugimura A., Tashiro K., Shimizu S.;
RT "Molecular cloning and expression of human hepatocyte growth factor.";
RL Nature 342:440-443(1989).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryonic fibroblast;
RC MEDLINE=91334393; PubMed=1831266;
RA Weidner K.M., Arakaki N., Hartmann G., Vandekerckhove J., Weingart S.,
RA Rieder H., Fomatsch C., Teubouchi H., Hishida T., Daikuhara Y.,
RA Birmeleier W.;
RT "Evidence for the identity of human scatter factor and human
RT hepatocyte growth factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
RN [6]
RP SEQUENCE FROM N.A.
RA Courtney L., Elliot G., Angell S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 249-695 FROM N.A.
RX MEDLINE=91369928; PubMed=1832556;
RA Miyazawa K., Kitamura A., Kitamura N.;
RT "Structural organization and the transcription initiation site of the
RT human hepatocyte growth factor gene.";
RL Biochemistry 30:9170-9176(1991).
RN [8]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=91207365; PubMed=1826837;
RA Yoshizawa Y., Arakaki N., Naka D., Takahashi K., Hirono S., Kondo J.,
RA Nakayama H., Gohda E., Kitamura N., Teubouchi H., Ishii T.,
RA Hishida T., Daikuhara Y.;
RT "Identification of the N-terminal residue of the heavy chain of both
RT native and recombinant human hepatocyte growth factor.";
RL Biochem. Biophys. Res. Commun. 175:660-667(1991).
RN [9]
RP CARBOHYDRATE-LINKAGE SITE THR-476.
RX MEDLINE=93129192; PubMed=1482348;
RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
RA Nakamura T., Shimizu S.;
RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
RT on the alpha chain.";

[1]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP STRAIN=Mistral; TISSUE=Liver;
 RC MEDLINE=90222197; PubMed=2139229;
 RA Toshio K., Hagiya M., Nishizawa T., Seki T., Shimonishi M.,
 Shimizu S., Nakamura T.;
 RT "Deduced primary structure of rat hepatocyte growth factor and
 expression of the mRNA in rat tissues";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistral; TISSUE=Liver;
 RX MEDLINE=91031482; PubMed=2146117;
 RA Okajima A., Miyazawa K., Kitamura N.;
 RT "Primary structure of rat hepatocyte growth factor and induction of
 its mRNA during liver regeneration following hepatic injury";
 RL Eur. J. Biochem. 193:375-381(1990).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 CC HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS
 CC AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
 CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 CC DISULFIDE BOND.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 4 kringle domains.
 CC -----
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 CC -----
 CC EMBL; D90102; BA14133.1; -;
 CC EMBL; X59400; CA36266.1; -;
 CC PIR; A35644; A35644.
 CC HSSP; P14210; 1BHT.
 CC MEROPS; S01.978; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_Ap; 1.
 DR SMART; SM00020; Tryp_Sec; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS00070; KRINGLE_2; 4.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 KM Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
 KW signal; Fyrtiolidone carboxylic acid.
 FT SIGNAL 1
 FT CHAIN 32
 FT CHAIN 495
 FT CHAIN 728
 FT MOD_RES 33
 FT DOMAIN 33
 FT DOMAIN 128
 FT DOMAIN 129
 FT DOMAIN 207
 FT DOMAIN 212
 FT DOMAIN 289
 FT DOMAIN 306
 FT DOMAIN 384
 FT DOMAIN 392
 FT DOMAIN 470
 FT DOMAIN 496
 FT DISULFID 71
 FT DISULFID 97
 FT DISULFID 75
 FT DISULFID 85
 FT DISULFID 488
 FT CARBOHYD 295

FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 656 656 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 728 AA; 82905 MW; 3E0BF1F96ADCEBFF CRC64;
 Query Match 46.4%; Score 250; DB 1; Length 728;
 Best Local Similarity 47.6%; Pred. No. 26-18;
 Matches 39; Conservative 11; Mismatches 32; Indels 0; Gaps 0;
 QY 7 DCHGGRSRYGSSITVTYGRTCQSSSWIPIPHQRTPEYVAGLTENYCRNPSGKQP 66
 DB 211 ECWTCGSSYRGPMQHTESGKTCQRWDQGTFRHKKFLPERYDKGDDNYCRNPSGKRP 270
 QY 67 WCYTTDPCVMEYCNLTQCSST 88
 DB 271 WCYTTDPCVMEYCAIKMCAHS 292
 RESULT 12
 HGF_MOUSE STANDARD; PRT; 728 AA.
 ID HGF_MOUSE
 AC Q08048; O61662; O64007;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 DE (Hepatopoietin A).
 GN HGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND SEQUENCE OF 496-504.
 RC TISSUE=Mammary fibroblast;
 RX MEDLINE=94183257; PubMed=8135822;
 RA Sasaki M., Nishio M., Sasaki T., Enami J.;
 RT "Identification of mouse mammary fibroblast-derived mammary growth
 RT factor as hepatocyte growth factor";
 RL Biochem. Biophys. Res. Commun. 199:772-779(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94363381; PubMed=8081873;
 RA Lee C.C., Kozak C.A., Yamada K.M.;
 RT "Structure, genetic mapping, and expression of the mouse Hgf/scatter
 RT factor gene";
 RL Cell Adhes. Commun. 1:101-111(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94060105; PubMed=8241272;
 RA Liu Y., Michalopoulos G.K., Zarnegar R.;
 RT "Molecular cloning and characterization of cDNA encoding mouse
 RT hepatocyte growth factor";
 RL Biochim. Biophys. Acta 1216:299-303(1993).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 CC HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS AS
 CC GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES. IT
 CC HAS NO DETECTABLE PROTEASE ACTIVITY.
 CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 CC DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=Q08048-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=Q08048-2; Sequence=VSP_005408;
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 4 kringle domains.
 CC -----
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DR EMBL; D10212; BAA01064.1; -
 DR EMBL; D10213; BAA01065.1; -
 DR EMBL; S71816; AAB31855.1; -
 DR EMBL; X72307; CAA51054.1; ALT_INIT.
 DR PIR; J02117; A60185.
 DR HSSP; P14210; 1BHT.
 DR MEROPS; S01.982; -
 DR MGD; MGI:96079; Hgf.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR01254; Ser.protease_Try.
 DR Pfam; PF00051; kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS0070; KRINGLE_2; 4.
 DR PROSITE; PS0240; TRYPsin DOM; 1.
 DR Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
 KW Signal; Alternative splicing; Pyrolydine carboxylic acid.
 FT SIGNAL 1 32
 FT CHAIN 33 495
 FT CHAIN 496 728
 FT MOD_RES 33 33
 FT DOMAIN 33 128
 FT DOMAIN 129 207
 FT DOMAIN 212 289
 FT DOMAIN 306 384
 FT DOMAIN 392 470
 FT DOMAIN 496 728
 FT DISULFID 71 97
 FT DISULFID 75 85
 FT DISULFID 488 607
 FT CARBOHYD 295 295
 FT CARBOHYD 403 403
 FT CARBOHYD 569 569
 FT CARBOHYD 656 656
 FT VARSPLIC 163 167
 FT CONFLICT 344 344
 FT CONFLICT 479 479
 FT CONFLICT 564 564
 FT CONFLICT 564 564
 SQ SEQUENCE 728 AA; 82944 MW; A0381FC497534328 CRC64;

Query Match 46.2%; Score 249; DB 1; Length 728;
 Best Local Similarity 47.6%; Pred. No. 2.6e-18;
 Matches 39; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

QY 7 DCHGGRGRRVRSSTTVVGRTRQSSSMIPHHQGTQPPNYPAAGLTENYCNRPDSGKRP 66
 DB 211 ECHTNGESYRGMDHTSGKTCQWDQOTPHRHKFLPERYPDKGPDVYCRNPDGKRP 270
 QY 67 WCYTDPVWEXECNLTCCSET 88
 DB 271 WCYTDPVWEXECNLTCCSET 292

RESULT 13
 HGFL_MOUSE

ID HGFL_MOUSE STANDARD; PRT; 716 AA.
 AC P26928;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hepatocyte growth factor-like protein precursor (Macrophage
 DE stimulatory protein) (MSP).
 GN MST1 OR HGFL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=92002017; PubMed=1832957;
 RA Friesner Degen S.J., Stuart L.A., Han S., Jamison C.S.;
 RT "Characterization of the mouse cDNA and gene coding for a hepatocyte
 RT growth factor-like protein: expression during development.";
 RL Biochemistry 30:9781-9791(1991).
 CC -1 FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
 CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
 CC CONSERVED.
 CC -1 TISSUE SPECIFICITY: LIVER. LOWER LEVELS IN LUNG, PLACENTA AND
 CC ADRENAL.
 CC -1 DEVELOPMENTAL STAGE: IS EXPRESSED AT LOW LEVELS DURING GESTATION.
 CC JUST BEFORE BIRTH THE LEVEL INCREASES DYNAMICALLY AND REMAINS
 CC STABLE AFTERWARDS.
 CC -1 PTM: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE
 CC HEID TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE
 CC POLYPEPTIDES.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1 SIMILARITY: Contains 4 kringle domains.
 CC -----
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FT DOMAIN 292 370 KRINGLE 3.
FT DOMAIN 379 457 KRINGLE 4.
FT DISULFID 489 716 SERINE PROTEASE-LIKE.
FT DISULFID 56 78 BY SIMILARITY.
FT DISULFID 60 66 BY SIMILARITY.
FT DISULFID 110 186 BY SIMILARITY.
FT DISULFID 131 169 BY SIMILARITY.
FT DISULFID 157 181 BY SIMILARITY.
FT DISULFID 191 268 BY SIMILARITY.
FT DISULFID 194 333 INTERCHAIN (BY SIMILARITY).
FT DISULFID 212 251 BY SIMILARITY.
FT DISULFID 240 263 BY SIMILARITY.
FT DISULFID 292 370 BY SIMILARITY.
FT DISULFID 313 352 BY SIMILARITY.
FT DISULFID 341 364 BY SIMILARITY.
FT DISULFID 379 457 BY SIMILARITY.
FT DISULFID 400 440 BY SIMILARITY.
FT DISULFID 428 452 BY SIMILARITY.
FT DISULFID 477 593 INTERCHAIN (BY SIMILARITY).
FT DISULFID 512 528 BY SIMILARITY.
FT DISULFID 607 672 BY SIMILARITY.
FT DISULFID 637 651 BY SIMILARITY.
FT DISULFID 662 690 BY SIMILARITY.
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19 19 P -> Q (IN GENOMIC SEQUENCE).
SQ SEQUENCE 716 AA; 80588 MW; BHCED2EP85213ACC CRC64;

Query Match 44.8%; Score 241.5; DB 1; Length 716;
Best Local Similarity 49.4%; Pred. No. 1.5e-17;
Matches 43; Conservative 9; Mismatches 34; Indels 1; Gaps 1;

Qy 4 VVDDCYHGDRSYRGISSTVTGRTQSWSSMTPHMQRTPEYVPAAGLTENYCRNPDSDG 63
Db 375 VPGCYHGSGEQYGVSKTRKGVQCCHWSETPHKQFPPTSPAPQGLEANFCRNDGD 434
Qy 64 KQ-PMCTTDPICVMEYCNLTQCSSE 89
Db 435 SHGPWCYTLDPDILFDYCALQRCDDQ 461

RESULT 14
PLAN_SHEEP STANDARD; PRT; 343 AA.
ID PLAN_SHEEP STANDARD; PRT; 343 AA.
AC P81286;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN Plg.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RX MEDLINE=9314995; Pubmed=1492092;
RA Schaller J., Straub C., Kamper U., Rickli B.E.;
RT "Complete amino acid sequence of ovine miniplasminogen.";
RL Protein Seq. Data Anal. 5:21-25(1992).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAAFIAN FOLLICLE. IT ACTIVATES THE URICINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C3. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble

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CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains at least 2 kringle domains.
DR PIR; B61545; B61545.
DR HSP; P00747; SHPG.
DR MEROPS; S01.233; -.
DR Interpro; IPR001314; Chymotrypsin.
DR Interpro; IPR000001; Kringle.
DR Interpro; IPR003966; Prothrombin.
DR Interpro; IPR001254; Ser protease_Try.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR Prodom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TRY_Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
FT NON_TER 1 1
FT DOMAIN <1 140 HEAVY CHAIN A.
FT DOMAIN 141 >343 LIGHT CHAIN A.
FT DOMAIN <1 17 KRINGLE 4.
FT DOMAIN 41 120 KRINGLE 5.
FT DOMAIN 114 341 SERINE PROTEASE.
FT ACT SITE 181 181 CHARGE RELAY SYSTEM.
FT ACT SITE 224 224 CHARGE RELAY SYSTEM.
FT ACT SITE 319 319 CHARGE RELAY SYSTEM.
FT NON_TER 343 343
SQ SEQUENCE 343 AA; 37662 MW; 8DFEB9A2D05966E0 CRC64;

Query Match 43.8%; Score 236; DB 1; Length 343;
Best Local Similarity 47.8%; Pred. No. 2.6e-17;
Matches 43; Conservative 13; Mismatches 32; Indels 2; Gaps 2;

Qy 1 KSPVDDCYHGDRSYRGISSTVTGRTQSWSSMTPHMQ-RTPEYVPAAGLTENYCRN 59
Db 8 ENPEADCMIGIGKGRKATTVAGVPCQEMAAQEPHRRGIFTPTNPRAGLEKNYCRN 67
Qy 60 PDGK-KQPMCTTDPICVMEYCNLTQCSSE 88
Db 68 PDGDNVPMCTTNPRAKLPDYCDIPCESS 97

RESULT 15
HGFL_HUMAN STANDARD; PRT; 711 AA.
ID HGFL_HUMAN STANDARD; PRT; 711 AA.
AC P26927; Q13350; Q14870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP) (Macrophage stimulating protein).
GN MST1 OR HGFL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RX MEDLINE=92002016; Pubmed=1655021;

```

RA Han S., Stuart L.A., Friezen Degen S.J.;
 RT "Characterization of the DNFI52 locus on human chromosome 3:
 RT identification of a gene coding for four kringle domains with
 RT homology to hepatocyte growth factor.";
 RL Biochemistry 30:9768-9780(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93340141; PubMed=8393443;
 RA Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
 RT "Cloning, sequencing, and expression of human macrophage stimulating
 RT protein (MSP, MST1) confirms MSP as a member of the family of kringle
 RT proteins and locates the MSP gene on chromosome 3.";
 RL J. Biol. Chem. 268:15461-15468(1993).
 CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
 CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
 CC CONSERVED.
 CC -1- PTM: MAY BE CLEAVED AFTER AA 484, TO YIELD A TWO-CHAIN MOLECULE
 CC HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEPARATE POLYPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 4 kringle domains.
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 DR EMBL; M74178; AAA50165.1; -;
 DR EMBL; U37055; AAC50471.1; -;
 DR EMBL; L11924; AAA59872.1; -;
 DR PIR; A40331; A47136.
 DR HSSP; P00747; 2PK4.
 DR MEROPS; S01.975; -;
 DR Genew; HGNC:7380; MST1.
 DR MIM; 142408; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser.protease_Try.
 DR Pfam; PF00051; kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR PRODOM; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRY_PSP; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS00070; KRINGLE_2; 4.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal;
 KW Polymorphism.
 FT SIGNAL 1 18
 FT CHAIN 19 711
 FT DOMAIN 32 109
 FT DOMAIN 110 186
 FT DOMAIN 191 268
 FT DOMAIN 283 361
 FT DOMAIN 370 448
 FT DOMAIN 484 711
 FT DISULFID 56 78
 FT DISULFID 60 66
 FT DISULFID 110 186
 FT DISULFID 131 169
 FT DISULFID 157 181
 FT DISULFID 191 268
 FT POTENTIAL.
 FT HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
 FT PAD.
 FT KRINGLE 1.
 FT KRINGLE 2.
 FT KRINGLE 3.
 FT KRINGLE 4.
 FT SERINE PROTEASE-LIKE.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.

FT DISULFID 194 324 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 212 251 BY SIMILARITY.
 FT DISULFID 240 263 BY SIMILARITY.
 FT DISULFID 283 361 BY SIMILARITY.
 FT DISULFID 304 343 BY SIMILARITY.
 FT DISULFID 332 355 BY SIMILARITY.
 FT DISULFID 370 448 BY SIMILARITY.
 FT DISULFID 391 431 BY SIMILARITY.
 FT DISULFID 419 443 BY SIMILARITY.
 FT DISULFID 468 588 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 507 523 BY SIMILARITY.
 FT DISULFID 602 667 BY SIMILARITY.
 FT DISULFID 632 646 BY SIMILARITY.
 FT DISULFID 657 685 BY SIMILARITY.
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 13 13 Y->C.
 FT VARIANT 13 13 /FTID=VAR_006631.
 FT VARIANT 212 212 C->F.
 FT VARIANT 212 212 /FTID=VAR_006632.
 FT VARIANT 676 676 E->K (IN dbSNP:7798).
 FT VARIANT 676 676 /FTID=VAR_014569.
 FT CONFLICT 623 623 L->F (IN REF.2).
 FT SEQUENCE 711 AA; 80379 MW; 596ED21F180290E4 CRC64;
 SQ
 Query Match 42.9%; Score 231.5; DB 1; Length 711;
 Best Local Similarity 49.4%; Pred. No. 1.6e-16;
 Matches 42; Conservative 10; Mismatches 32; Indels 1; Gaps 1;
 QY 6 ODCHGDRSYRGISSTVTGRTQSWSSMIDPHMQRTPPENYPNAGLTENYCRNPDGSKQ 65
 DB 368 QDCYHAGRGYRGVGTGSKTRKGVQCQRMWSAETPHKQFTFTSEPHQLEENFCRNPDGDSH 427
 QY 66 -PWCYTTDPCTWMEYCNLTQCSETE 89
 DB 428 GPWCYTMDFRTPFDYCALRCADDQ 452

Search completed: January 12, 2004, 17:23:57
 Job time : 8.86842 secs

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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:18:07 ; Search time 29.0769 Seconds
(without alignments)
807.553 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539
Sequence: 1 KSPVVDQCHGDGRSYRGIS.....DPCVRWEYCNLTQCSSESG 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvivirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	539	100.0	113	4	Q9U1R6
2	424	78.7	113	4	Q9U1R7
3	423	78.5	810	4	Q15146
4	422	78.3	105	4	Q9U1R8
5	413	76.6	454	6	Q46506
6	409	75.9	113	4	Q9U1R5
7	392	72.7	359	6	Q8WVR1
8	391	72.5	145	6	Q28911
9	388	72.0	812	11	Q91WJ5
10	380	70.5	132	4	Q16609
11	366.5	68.0	812	11	Q9R0W3
12	366	67.9	806	6	Q18783
13	281	52.1	2869	6	Q28398
14	272	50.5	429	13	Q8AVB0
15	258.5	48.0	947	13	Q8AXY6
16	252	46.8	285	4	Q8TCE2

17	252	46.8	290	4	Q02935	Q02935 homo sapien
18	251	46.6	334	6	Q46507	Q46507 papio hamad
19	250.5	46.5	710	13	Q91402	Q91402 xenopus. he
20	250	46.4	728	11	Q8C9G5	Q8C9G5 mus musculu
21	249.5	46.3	946	13	Q07153	Q07153 torpedo cal
22	249.5	46.3	948	5	Q9Y1Y6	Q9Y1Y6 ephydalia f
23	248.5	46.1	209	11	Q8BS17	Q8BS17 mus musculu
24	248.5	46.1	313	13	Q9PU78	Q9PU78 crocodylus
25	247.5	45.9	296	4	Q14519	Q14519 homo sapien
26	246	45.6	717	13	P70006	P70006 xenopus lae
27	244	45.3	716	13	Q91691	Q91691 xenopus lae
28	243	45.1	728	6	Q9BH09	Q9BH09 felis silve
29	242.5	45.0	208	4	Q9BYM0	Q9BYM0 homo sapien
30	242.5	44.8	210	4	Q13494	Q13494 homo sapien
31	241.5	44.8	716	11	Q91XG8	Q91XG8 mus musculu
32	238.5	44.2	716	11	P70521	P70521 rattus norv
33	237.5	44.1	109	6	Q9N1B8	Q9N1B8 ovris aries
34	236.5	43.9	709	13	Q90ZN6	Q90ZN6 brachydantio
35	236	43.8	53	4	Q9UM12	Q9UM12 homo sapien
36	236	43.8	704	13	Q90865	Q90865 gallus gall
37	232.5	43.1	211	11	Q55027	Q55027 mus musculu
38	232.5	43.1	385	5	Q25101	Q25101 herdmania m
39	232	43.0	726	13	Q90978	Q90978 gallus gall
40	231.5	42.9	215	13	Q42341	Q42341 gallus gall
41	227.5	42.2	567	4	Q13208	Q13208 homo sapien
42	226.5	42.0	648	4	Q9H1V4	Q9H1V4 homo sapien
43	219	40.6	95	4	Q8N696	Q8N696 homo sapien
44	207.5	38.5	90	4	Q8NG20	Q8NG20 homo sapien
45	203.5	37.8	930	13	Q8AV69	Q8AV69 xenopus lae

ALIGNMENTS

RESULT 1
ID Q9U1R6 PRELIMINARY; PRT; 113 AA.
AC Q9U1R6;
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
GN APOA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2181705; PubMed=11285247;
RA Ogortelkova M., Kraft H.G., Ehnholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL, AF158661; AAF03679.1; JOINED.
DR EMBL, AF158660; AAF03679.1; JOINED.
DR HSP, P00747; 2PK4.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PRINTS; PR000195; KRINGLE.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR GLYCOPTREIN; Kringle; Lipoprotein.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12697 MW; 51D4461D9C66312E CRC64;
Query Match 100.0%; Score 539; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1e-52;


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Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSPVDDCYHGDRSRGISTTGTTCOSWSSMTPHMHQRTPEYNNAGLTENYCRNP 60
DB 4 KSPVDDCYHGDRSRGISTTGTTCOSWSSMTPHMHQRTPEYNNAGLTENYCRNP 63
QY 61 DSGKQPCWCTTDPCEVMEYCNLTQCSETESG 91
DB 64 DSGKQPCWCTTDPCEVMEYCNLTQCSETESG 94

RESULT 2
Q9UR7 PRELIMINARY; PRT; 113 AA.
AC Q9UR7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ogorolkova M., Krat H.G., Enholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT types 6 to 10 domain affect lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians.";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158659; AAF03678.1; JOINED.
DR HSSP; P00747; 2PK4.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle.1.
DR SMART; SM00130; KR.1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal.
FT CHAIN 1 19 PLASMINOGEN.
FT SIGNAL 1 19
SQ SEQUENCE 113 AA; 12815 MW; 4F80ADP8708548CB CRC64;

Query Match 78.7%; Score 424; DB 4; Length 113;
Best Local Similarity 78.9%; Pred. No. 7, 4e-40;
Matches 71; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
QY 1 KSPVDDCYHGDRSRGISTTGTTCOSWSSMTPHMHQRTPEYNNAGLTENYCRNP 60
DB 4 KSPVDDCYHGDRSRGISTTGTTCOSWSSMTPHMHQRTPEYNNAGLTENYCRNP 63
QY 61 DSGKQPCWCTTDPCEVMEYCNLTQCSETES 90
DB 64 DSGKQPCWCTTDPCEVMEYCNLTQCSETES 93

RESULT 3
Q15146 PRELIMINARY; PRT; 810 AA.
AC Q15146;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Plasminogen precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
RA Mitchell D., Robinson J.H.;
RT "Expression of recombinant human plasminogen and aglycoplasminogen in
RT HeLa cells.";
RL Fibrinolysis 0:0-0(1991).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL; M74220; AAA36451.1; -.
DR HSSP; P00747; 2PK4.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan. app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR.5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPE; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal.
FT CHAIN 1 19 PLASMINOGEN.
FT SIGNAL 1 19
SQ SEQUENCE 810 AA; 90555 MW; B05C7DAB0D020B3C CRC64;

Query Match 78.5%; Score 423; DB 4; Length 810;
Best Local Similarity 78.7%; Pred. No. 8, 2e-39;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 2 SPVDDCYHGDRSRGISTTGTTCOSWSSMTPHMHQRTPEYNNAGLTENYCRNP 61
DB 371 TPVDDCYHGDRSGSYRGISTTGTTCOSWSSMTPHMHQRTPEYNNAGLTENYCRNP 430
QY 62 DSGKQPCWCTTDPCEVMEYCNLTQCSETES 90
DB 431 ADKQPCWCTTDPCEVMEYCNLTQCSETES 459

RESULT 4
Q9UR8 PRELIMINARY; PRT; 105 AA.
AC Q9UR8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21181705; PubMed=11285247;
RA Ogorolkova M., Krat H.G., Enholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT types 6 to 10 domain affect lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians.";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158656; AAF03677.1; -.

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DR EMBL; AF158655; AAF03677.1; JOINED.
 DR HSP; P00747; 2PKA.
 DR InterPro: IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 SQ SEQUENCE 105 AA; 11882 MW; 6ECB6C02CD30EFA2 CRC64;

Query Match 78.3%; Score 422; DB 4; Length 105;
 Best Local Similarity 80.0%; Pred. No. 1.2e-39;
 Matches 72; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

QY 1 KSPVQDCYHGDGRSYRGISSTVTGRTQGSWSSMIPMHQRTPEPNYAGLTENYCRNP 60
 DB 4 QSPGVQDCYHGDGRSYRGISSTVTGRTQGSWSSMIPMHQRTPEPNYAGLTENYCRNP 63
 QY 61 DSGKQPCYTTDPCVMEYCNLTQCSETE 90
 DB 64 DAISPCYTMDBPVMEYCNLTQCSETE 93

RESULT 5
 ID 046506 PRELIMINARY; PRT; 454 AA.
 AC 046506;
 DT 01-JUN-1998 (TRENBLREL. 06, Created)
 DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Apolipoprotein a (Fragment).
 GN BABAPOA.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 NCBI_TaxID=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cox L.A., Jett C., Haxson J.E.;
 RT Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
 RT Site Mutation is Associated with Deletion of a Single Exon in a Null
 RT Allele.
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 DR EMBL; AF029691; AAB97886.1; -.
 DR HSP; P00747; 2PKA.
 DR MEROPS; S01.999; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRODOM; PD000395; Kringle; 2.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; TRY_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Glycoprotein; Hydrolyase; Kringle; Lipoprotein; Protease;
 KW Serine protease.
 FT NON_TER 1
 SQ SEQUENCE 454 AA; 50041 MW; 974B30744C187B2F CRC64;
 Query Match 76.6%; Score 413; DB 6; Length 454;

Best Local Similarity 77.5%; Pred. No. 5.7e-38;
 Matches 69; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 QY 1 KSPVQDCYHGDGRSYRGISSTVTGRTQGSWSSMIPMHQRTPEPNYAGLTENYCRNP 60
 DB 95 QSPGVQDCYHGDGRSYRGISSTVTGRTQGSWSSMIPMHQRTPEPNYAGLTENYCRNP 154
 QY 61 DSGKQPCYTTDPCVMEYCNLTQCSETE 89
 DB 155 DADTGPWCFTMDPSVMEYCNLTQCSETE 163

RESULT 6
 ID 09UR5 PRELIMINARY; PRT; 113 AA.
 AC 09UR5;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Apolipoprotein (a) (Fragment).
 GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2181705; PubMed=11285247;
 RA Ogorekova M., Kraft H.G., Ehmholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
 RT types 6 to 10 domain affect lip(a) plasma concentrations and have
 RT different patterns in Africans and Caucasians."
 RL Hum. Mol. Genet. 10:815-824 (2001).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; AF158663; AAF03680.1; -.
 DR EMBL; AF158662; AAF03680.1; JOINED.
 DR HSP; P00747; 1PMK.
 DR InterPro: IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 113 AA; 12685 MW; F3D65681D9B5253A CRC64;
 Query Match 75.9%; Score 409; DB 4; Length 113;
 Best Local Similarity 75.3%; Pred. No. 3.5e-38;
 Matches 67; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 KSPVQDCYHGDGRSYRGISSTVTGRTQGSWSSMIPMHQRTPEPNYAGLTENYCRNP 60
 DB 4 QTPVVRQCYHGDGRSYRGISSTVTGRTQGSWSSMIPMHQRTPEPNYAGLTENYCRNP 63
 QY 61 DSGKQPCYTTDPCVMEYCNLTQCSETE 89
 DB 64 DADTGPWCFTMDPSVMEYCNLTQCSETE 92

RESULT 7
 ID 08WRI PRELIMINARY; PRT; 359 AA.
 AC 08WRI;
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Plasminogen (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

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OX NCB1_TaxID=9615;
RN [1]
RA SEQUENCE FROM N.A.
RA Flier-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,
RT Folman J., Waters D.J.
RT "Angiostatin is detectable in the urine of dogs with spontaneous Bone
RT Cancer."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL: A1069985; A158519.1; -.
DR InterPro: IPR000001; Kringle.
DR Pfam: PF00051; Kringle; 4.
DR PRINTS: PR00018; KRINGLE.
DR PRODOM: PD000395; Kringle; 4.
DR SMART: SM00130; KR; 4.
DR PROSITE: PS00021; KRINGLE_1; 4.
DR PROSITE: PS50070; KRINGLE_2; 4.
KW Glycoprotein; Kringle.
FT NON_TER 1 359
SQ SEQUENCE 359 AA; 41172 MW; 776035F4AB0BDD9E CRC64;

Query Match 72.7%; Score 392; DB 6; Length 359;
Best Local Similarity 72.9%; Pred. No. 9.9e-36;
Matches 62; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 KSPVDDCYHGGRSYRGISSTVTGRTCSWSSMTPHMHORTPENYPNAGLTENYCRNP 60
DB 275 QTPVDDCYHGGRSYRGISSTVTGRTCSWSSMTPHMHORTPENYPNAGLTENYCRNP 334

QY 61 DSGKOPWCYTTDPCVREYCNLTQC 85
DB 335 DADKSPWCYTTDPSVRWEFCNLKRC 359

RESULT 8
Q28911 PRELIMINARY; PRT; 145 AA.
ID Q28911;
AC Q28911;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Apolipoprotein[a] (Fragment).
GN APOLIPOPROTEIN[a].
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9339387; PubMed=7666007;
RA Ramharack R., Spahr M.A., Hicks G.W., Kieft K.A., Brammer D.W.,
RA Minton L.L., Newton R.S.
RT "gemfibrozil significantly lowers cynomolgus monkey plasma
RT lipoprotein[a]-protein and liver apolipoprotein[a] mRNA levels."
RL J. Lipid Res. 36:1294-1304 (1995).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL: S79621; AAD14312.1; -.
DR HSSP: P00747; 2PK4.
DR InterPro: IPR000001; Kringle.
DR Pfam: PF00051; Kringle; 1.
DR PRINTS: PR00018; KRINGLE.
DR PRODOM: PD000395; Kringle; 1.
DR SMART: SM00130; KR; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS50070; KRINGLE_2; 1.
KW Glycoprotein; Kringle; Lipoprotein.
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16097 MW; 0D2DA20A06A5D87 CRC64;

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Query Match 72.5%; Score 391; DB 6; Length 145;
Best Local Similarity 75.3%; Pred. No. 4.8e-36;
Matches 67; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 KSPVDDCYHGGRSYRGISSTVTGRTCSWSSMTPHMHORTPENYPNAGLTENYCRNP 60
DB 36 QSHVDDCYHGGRSYRGISSTVTGRTCSWSSMTPHMHORTPENYPNAGLTENYCRNP 95

QY 61 DSGKOPWCYTTDPCVREYCNLTQCSETE 89
DB 96 DPVAAPCYTTPBNPVRWEYCNLTQCSDAE 124

RESULT 9
Q91WJ5 PRELIMINARY; PRT; 812 AA.
ID Q91WJ5;
AC Q91WJ5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Plasminogen.
GN PLG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Brattwalte M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA Nagaraja R.;
RT "Genomic Sequence Analysis in the Mouse t-complex Region."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL: BC014773; AAH14773.1; -.
DR EMBL: AF481053; AAM22156.1; -.
DR HSSP: P00761; 1AN1.
DR MGD: MGI:97620; P19.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00051; Kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR PRODOM: PD000395; Kringle; 5.
DR PROSITE: PS00021; KRINGLE_1; 5.
DR PROSITE: PS50070; KRINGLE_2; 5.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolyase; Kringle; Protease; Serine protease.
SQ SEQUENCE 812 AA; 90781 MW; 24173260E6A2FED2 CRC64;

Query Match 72.0%; Score 388; DB 11; Length 812;
Best Local Similarity 70.5%; Pred. No. 6.7e-35;
Matches 62; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 1 KSPVDDCYHGGRSYRGISSTVTGRTCSWSSMTPHMHORTPENYPNAGLTENYCRNP 60
DB 370 QTPVDDCYHGDGQSYRGISSTVTGRTCSWSSMTPHMHORTPENYPNAGLTENYCRNP 429

```

QY 61 DSGKQPCYTTDPCVMEYCNLTQCSCT 88
 DB 430 DGDGKPCYTTDPCVMEYCNLTQCSCT 457

RESULT 10

Q16609 PRELIMINARY; PRT; 132 AA.

AC 016609; 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 RT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE (APOARGC).
 OS APOARGC.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 RN 1) SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95268939; PubMed=7749817;
 RA Byrne C.D., Schwartz K., Lawn R.M.,
 RT "Loss of a splice donor site at a 'skipped exon' in a gene homologous
 RT to apolipoprotein(a) leads to an mRNA encoding a protein consisting of
 RT a single kringle domain."
 RT Arterioscler. Thromb. Vasc. Biol. 15:65-70(1995).
 RL -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC EMBL; U19518; AAA85692.1; -;
 DR EMBL; U19517; AAA85692.1; -;
 DR HSSP; P00747; 1PMK.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; Kringle.1.
 DR PRINTS; PR00018; KRINGLE.
 DR PRODOM; PD000395; Kringle.1.
 DR SMART; SM00130; KR.1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 KW Glycoprotein; Kringle.
 SQ SEQUENCE 132 AA; 1486 MW; 3794AD30A586DBA CRC64;

Query Match 70.5%; Score 380; DB 4; Length 132;
 Best Local Similarity 72.4%; Pred. No. 7.3e-35;

Matches 63; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 3 PNVQDCYHGDGSRYSSTTTGRTQSWSMIPMHQRTPEYCNLTQCSCT 62
 DB 23 PSVQDCYHSGOSYRGTYFTTGTGTCQAWSSMTPHQSHSTPEKYNPDGLISNYCRNPD 82
 QY 63 GKPQPCYTTDPCVMEYCNLTQCSCT 89
 DB 83 SAGPWCYTTDPCVMEYCNLTQCSCT 109

RESULT 11

Q090W3 PRELIMINARY; PRT; 812 AA.

AC 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 RT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Plasminogen protein precursor (EC 3.4.21.7).
 OS PLASMINOGEN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=10116;
 RN 1) SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Bangerter K., Johnson A.H., Thorsen S.;
 RT "Rat plasminogen: cDNA and gene structure."
 RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91250378; PubMed=1645711;
 RA Kanalas J.O., Macker S.P.;
 RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
 RT receptor site for plasminogen."
 RL J. Biol. Chem. 266:10825-10829(1991).
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 DR EMBL; AJ242649; CAB46014.1; -;
 DR HSSP; P00747; 1PMK.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan app.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR001400; Somatostatin.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRODOM; PD000395; PROTHROMBIN.
 DR SMART; SM00130; KR.4.
 DR SMART; SM00473; PAN_AP.1.
 DR SMART; SM00020; Tryp_Spec.1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00338; SOMATOSTATIN_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM.1.
 DR PROSITE; PS00134; TRYPSIN_HIS.1.
 DR PROSITE; PS00135; TRYPSIN_SER.1.
 KW Glycoprotein; Hydrolyase; Kringle; Protease; Serine protease; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 812 PLASMINOGEN.
 SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410BCE9E CRC64;

Query Match 68.0%; Score 366.5; DB 11; Length 812;
 Best Local Similarity 66.3%; Pred. No. 1.7e-32;

Matches 61; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

QY 1 KSPVQDCYHGDGSRYSSTTTGRTQSWSMIPMHQRTPEYCNLTQCSCT 60
 DB 369 QTPVQDCYHGDGSRYSSTTTGRTQSWSMIPMHQRTPEYCNLTQCSCT 428
 QY 61 DSGKQPCYTTDPCVMEYCNLTQCSCT 89
 DB 429 DNDGKPCYTTDPCVMEYCNLTQCSCT 460

RESULT 12

Q18783 PRELIMINARY; PRT; 806 AA.

AC 018783; 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 RT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Plasminogen.
 OS Plasminogen.
 OS Macropus eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 NCBI_Taxid=9315;
 RN 1) SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98004511; PubMed=9342350;
 RA Lawn R.M., Schwartz K., Patchy L.;
 RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog."
 RT Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 DR EMBL; AF012297; AAB65760.1; -;

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DR HSSP; P00747; SHPG.
DR MEROPS; S01.233; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser protease_Try.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR GlycoProtein; Hydrolyase; Kringle; Protease; Serine protease.
KW GlycoProtein; Hydrolyase; Kringle; Protease; Serine protease.
SQ SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;

Query Match 67.9%; Score 366; DB 6; Length 806;
Best Local Similarity 63.3%; Pred. No. 1.9e-32;
Matches 57; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 KSPVQDCYHGDGSRYSIGSTVTYTGRTQSWSMIPHHQRTPEPNYPNAGLTENYCRNP 60
Db 364 QSVIVGECYCKGNKENTVGTSTTISGKKQAMSMTHQKKIPDNPENADLRNYCRNP 423
Qy 61 DSGKQPCYCTTDPCCVMEYCNLTQCSSTES 90
Db 424 DGDKSPWCYTMDDPTVMEFCNLKSCGTGS 453

RESULT 13
ID Q28398 PRELIMINARY; PRT; 2869 AA.
AC Q28398;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
OS Eritaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96025778; PubMed=7592597;
RA Lwin R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
RA Byrne C.D., Fong K.J., Meier K., Pathy L.;
RT "The recurring evolution of lipoprotein(a). Insights from cloning of
RT hedgehog apolipoprotein(a).";
RL J. Biol. Chem. 270:24004-24009(1995).
CC -1- SIMILARITY: CONTAINS 31 KRINGLE DOMAINS.
DR EMBL; U31170; AAC48522.1; -.
DR HSSP; P00747; SHPG.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 31.
DR ProDom; PD000395; Kringle; 31.
DR SMART; SM00130; KR; 31.
DR PROSITE; PS00021; KRINGLE_1; 30.
DR PROSITE; PS00070; KRINGLE_2; 31.
KW GlycoProtein; Kringle; Lipoprotein.
FT NON TER 1
SQ SEQUENCE 2869 AA; 318601 MW; 9527CEP985A4FB2A CRC64;

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Query Match 52.1%; Score 281; DB 6; Length 2869;
Best Local Similarity 51.7%; Pred. No. 2.4e-22;
Matches 45; Conservative 8; Mismatches 34; Indels 0; Gaps 0;

Qy 4 VVQDCYHGDGSRYSIGSTVTYTGRTQSWSMIPHHQRTPEPNYPNAGLTENYCRNPDSG 63
Db 2680 IPQDCLEGTGENTVGSVAATVSGHTQWRMEOSPHSHRTPENYPKNLFGNYCRNPDSG 2739
Qy 64 KQPCYCTTDPCCVMEYCNLTQCSSTES 90
Db 2740 VAPWCYTTNSAVRMEYCKIPSCNSSS 2766

RESULT 14
ID Q8AVB0 PRELIMINARY; PRT; 429 AA.
AC Q8AVB0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasminogen precursor (Fragment).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in teleostei:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIIa.";
RL Blood Cells Mol. Dis. 0:0-0(2002).
DR EMBL; AF515276; AAN71006.1; -.
FT NON TER 1
SQ SEQUENCE 429 AA; 47556 MW; 9A580A214A549C12 CRC64;

Query Match 50.5%; Score 272; DB 13; Length 429;
Best Local Similarity 51.1%; Pred. No. 3.1e-22;
Matches 47; Conservative 12; Mismatches 31; Indels 2; Gaps 2;

Qy 2 SPVQDCYHGDGSRYSIGSTVTYTGRTQSWSMIPHHQRTPEPNYPNAGLTENYCRNP 60
Db 96 APEKCKKNGALEYRGSTMTVGTQAMWSMTPHQAFTPEHPKGLSNCRCNP 155
Qy 61 DSG-KQPCYCTTDPCCVMEYCNLTQCSSTESG 91
Db 156 DSDVNGPCYCTTDPKSKMDYQIPDCSLKCG 187

RESULT 15
ID Q8AXY6 PRELIMINARY; PRT; 947 AA.
AC Q8AXY6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Muscle-specific receptor tyrosine kinase Musk.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20538710; PubMed=11083926;
RA Ip F.C., Glas D.G., Gies D.R., Cheung J., Lai K.O., Fu A.K.,
RA Vancopoulos G.D., Ip N.Y.;
RT "Cloning and characterization of muscle-specific kinase in chicken.";
RL Mol. Cell. Neurosci. 16:661-673(2000).
FT NON TER 12
SQ SEQUENCE FROM N.A.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:16:07 ; Search time 36.2632 Seconds
(without alignments)
398.314 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539

Sequence: 1 KSPVQDCHGDGSRYSRGIS.....DPCVMEYCNLTQCSSETS G 1

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues 1107863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	539	100.0	91	22	AAV72945
2	539	100.0	308	22	AAV72944
3	425	78.8	810	22	AA672248
4	423	78.5	280	20	AAV02108
5	423	78.5	297	20	AAV02103
6	423	78.5	361	20	AAV08687
7	423	78.5	363	21	AAV70255
8	423	78.5	364	20	AAV02106
9	423	78.5	364	21	AAV01905

10	423	78.5	369	21	AAV53868	Amino acid sequenc
11	423	78.5	374	21	AAV79226	Angiogenesis inhib
12	423	78.5	375	21	AAV79225	Angiogenesis inhib
13	423	78.5	378	17	AAV07579	Human kringlike 1-48
14	423	78.5	378	17	AAV16450	Human angiotensin
15	423	78.5	378	23	AAV48894	Human angiotensin
16	423	78.5	380	20	AAV02105	A multifunctional
17	423	78.5	381	20	AAV02101	A multifunctional
18	423	78.5	452	21	AAV79224	Angiogenesis inhib
19	423	78.5	453	21	AAV50501	Amino acid sequenc
20	423	78.5	458	23	ABV75941	Human plasminogen
21	423	78.5	467	13	AAV22499	[GARSVO] - [Plasmin
22	423	78.5	476	13	AAV22503	[GARSVO] - [Plasmin
23	423	78.5	484	24	AAV79749	Human plasminogen
24	423	78.5	563	23	ABV75942	Endothelial cell g
25	423	78.5	566	20	AAV02100	A multifunctional
26	423	78.5	571	23	ABV75944	Angiotensin-tumour
27	423	78.5	576	23	ABV75943	Angiotensin-tumour
28	423	78.5	790	15	AAV60519	Human 'Glu' plasmi
29	423	78.5	790	22	AAV36562	Mammalian kringli
30	423	78.5	791	18	AAV34285	Human plasminogen
31	423	78.5	791	21	AAV01887	Human plasminogen
32	423	78.5	791	21	AAV9589	Human plasminogen
33	423	78.5	791	21	AAV50867	Human plasminogen
34	423	78.5	791	22	AAV67223	Amino acid sequenc
35	423	78.5	791	22	AAV23660	Human plasminogen
36	423	78.5	791	24	ABV76087	Human plasminogen
37	423	78.5	807	13	AAV20012	PA mutant pig 1-54
38	423	78.5	810	11	AAV08065	Human plasminogen
39	423	78.5	810	12	AAV33219	RS61G human plasmi
40	423	78.5	810	12	AAV12406	RS61G human plasmi
41	423	78.5	810	12	AAV13220	Human plasminogen
42	423	78.5	810	12	AAV13221	Human plasminogen
43	423	78.5	810	12	AAV12938	Plasminogen mutcin
44	423	78.5	810	14	AAV34428	Sequence encoded p
45	423	78.5	810	18	AAV31169	Plasminogen protei

ALIGNMENTS

RESULT 1
ID AAV72945
AAV72945 standard; Protein; 91 AA.
AC AAV72945;
XX
XX
DT 13-JUN-2001 (first entry)
XX
DE Human apolipoprotein(a) kringlike domain IV36, LK6 protein.
XX
KW Human; angiogenesis inhibitor; LK6; apolipoprotein(a) kringlike domain;
KW angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy;
KW cytoskeletal; antithrombotic; antitumor; antiproliferative; psoriasis;
KW ocular angiogenic disease; endothelial cell proliferation; tumour;
KW cell migration.
XX
OS Homo sapiens.
XX
PN WO200119868-A1.
XX
PD 22-MAR-2001.
XX
PF 15-SEP-1999; 99WO-KR00554.
XX
PR 15-SEP-1999; 99WO-KR00554.
XX
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
XX
PI Chang J, Kim JS, Park EJ, Yum J, Chung S;
XX WPI; 2001-244787/25.
DR N-PSDB; AAD03256.

```

XX  Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
PT  diseases, e.g. cancer and rheumatoid arthritis, has human
PT  apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT  sequence -
PS  Claim 1: Page 44-45; 50pp; English.
XX
CC  The present sequence is human LK6 protein which contains the amino
CC  acid sequence of human apolipoprotein(a) kringle domain IV36 (LK6
CC  (KIV36)). The human apolipoprotein(a) kringle domains IV36 (LK6
CC  protein), IV37 (LK7 protein) and V38 (LK8 protein) together form the
CC  angiogenesis inhibitor, LK68 protein. LK68, LK6, LK7 and LK8 are
CC  inhibitors are of endothelial cell proliferation, cell migration and
CC  normal development of capillaries in the chick embryo chorioallantoic
CC  membrane (CAM). LK68 protein, its single kringles or their functional
CC  equivalents, are useful for treating angiogenesis-mediated diseases,
CC  such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
CC  disease in animals or humans. LK68 is useful as an anticancer agent and
CC  also for inhibiting primary tumour growth.
XX
SQ  Sequence 91 AA;
Query Match 100.0%; Score 539; DB 22; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSPVVDCHGDRSGSYRGISSTVTGRTQSWSSMIPHWORTPENYPNAGLTENYCRNP 60
DB 1 KSPVVDCHGDRSGSYRGISSTVTGRTQSWSSMIPHWORTPENYPNAGLTENYCRNP 60
QY 61 DSGKOPWCYTTDPCVMEYCNLTQCSSETS 91
DB 61 DSGKOPWCYTTDPCVMEYCNLTQCSSETS 91
RESULT 2
AA72944
ID AA72944 standard; Protein; 308 AA.
XX
AC AA72944;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human angiogenesis inhibitor, LK68 protein.
XX
KW Human; angiogenesis inhibitor; LK68; apolipoprotein(a) kringle domain;
KW angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy;
KW cytostatic; antirheumatic; antiarthritic; antipsoriatic; psoriasis;
KW ocular angiogenic disease; endothelial cell proliferation; tumour;
KW cell migration.
XX
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /note= "Apolipoprotein(a) kringle domain IV36, LK6
FT protein"
FT 119..207
FT /label= KIV37
FT /note= "Apolipoprotein(a) kringle domain IV37, LK7
FT protein"
FT 223..308
FT /label= KV38
FT /note= "Apolipoprotein(a) kringle domain V38, LK8
FT protein"
XX
XX WO200119868-A1.
XX
XX 22-MAR-2001.
XX
XX 15-SEP-1999; 99WO-KR00554.

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XX 15-SEP-1999; 99WO-KR00554.
XX
XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
PA
XX Chang J, Kim JS, Park EJ, Yum J, Chung S;
XX
XX WPI; 2001-244787/25.
DR N-PSDB; AAD03255.
XX
PT Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
PT diseases, e.g. cancer and rheumatoid arthritis, has human
PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT sequence -
XX
PS Claim 4: Page 42-44; 50pp; English.
XX
CC The present sequence is human angiogenesis inhibitor, LK68 protein.
CC LK68 protein contains the amino acid sequences of human apolipoprotein(a)
CC kringle domains IV36 (LK6 protein), IV37 (LK7 protein) and V38
CC (LK8 protein). LK68, LK6, LK7 and LK8 are inhibitors are of endothelial
CC cell proliferation, cell migration and normal development of capillaries
CC in the chick embryo chorioallantoic membrane (CAM). LK68 protein, its
CC single kringles or their functional equivalents, are useful for
CC treating angiogenesis-mediated diseases, such as cancer, rheumatoid
CC arthritis, psoriasis or ocular angiogenic disease in animals or humans.
CC LK68 is useful as an anticancer agent and also for inhibiting primary
CC tumour growth.
XX
SQ Sequence 308 AA;
Query Match 100.0%; Score 539; DB 22; Length 308;
Best Local Similarity 100.0%; Pred. No. 4.8e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSPVVDCHGDRSGSYRGISSTVTGRTQSWSSMIPHWORTPENYPNAGLTENYCRNP 60
DB 1 KSPVVDCHGDRSGSYRGISSTVTGRTQSWSSMIPHWORTPENYPNAGLTENYCRNP 60
QY 61 DSGKOPWCYTTDPCVMEYCNLTQCSSETS 91
DB 61 DSGKOPWCYTTDPCVMEYCNLTQCSSETS 91
RESULT 3
AAG67228
ID AAG67228 standard; Protein; 810 AA.
XX
AC AAG67228;
XX
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of monkey plasminogen.
XX
XX
XX Angiostatin; plasminogen; sulfydryl donor; angiogenesis; tumour;
KW angiogenic disease; neoplastic disease; connective tissue disorder;
KW rheumatoid arthritis; atherosclerosis; ocular angiogenic disease;
KW diabetic retinopathy; corneal graft rejection; cardiovascular disease;
KW cerebral vascular disease; diabetes; immune disorder;
KW chronic inflammation; autoimmunity.
XX
XX Macaca mulatta.
XX
XX WO200158921-A2.
XX
XX 16-AUG-2001.
XX
XX 08-FEB-2001; 2001WO-US04021.
XX
XX 08-FEB-2000; 2000US-0500397.
XX
XX (NOUN ) UNIV NORTHWESTERN.
XX

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DR	XX	WPI; 1999-255098/21.
PT	XX	New multifunctional proteins useful for treating angiogenic-mediated diseases
PS	XX	Claim 5; Page 103-104; 121pp; English.
CC	XX	The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the invention.
CC	XX	Sequence 280 AA;
CC	XX	Query Match 78.5%; Score 423; DB 20; Length 280;
CC	XX	Best Local Similarity 78.7%; Pred. No. 2,3e-31;
CC	XX	Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0
QY	QY	2 SPVWDCCYGGDGRSYRGISSTTVGRTCCQSSSMIPHQRTPEPNYCNAGLTENYCRNPP 61
DB	DB	192 TFOVDDCTHGGDSYRGISSTTTTGKCCQSSSMTPRHQRTPEPNYCNAGLTENYCRNPP 251
QY	QY	62 SGKOPWCYTTDPCVMEYCNLTQCSSETS 90
DB	DB	252 ADKGPWCFTTDPSPVMEYCNLTQCSSETS 280
RESULT 5		
ID	AA	AAV02103
ID	AA	AAV02103 standard; Protein; 297 AA.
AC	XX	AAV02103;
XX	XX	
DT	XX	16-JUL-1999 (fixed entry)
DE	XX	A multifunctional protein of the invention.
XX	XX	Angiostatin; endostatin; interferon; thrombospondin;
KW	KW	interferon-inducible protein; platelet factor 4; anti-angiogenic;
KM	KM	anti-tumor; multifunctional protein; angiogenic-mediated disease;
KW	KW	cancer; diabetic retinopathy; macular degeneration; arthritis;
XX	XX	tumor cell production.
XX	OS	Synthetic.
OS	OS	Homo sapiens.
XX	XX	WO9916889-A1.
PN	PN	
PD	PD	08-APR-1999.
XX	XX	
XX	XX	30-SEP-1998; 98WO-US20464.
PF	PF	
PR	PR	01-OCT-1997; 97US-0060609.
XX	XX	
PA	PA	(SEAR) SEARLE & CO G D.
XX	XX	
PI	PI	Bolanowski MA, Caparon MH, Casperson GF, Gregory SA;
PI	PI	Klein BK, McKearn JP;
XX	XX	
DR	XX	WPI; 1999-255098/21.
XX	XX	New multifunctional proteins useful for treating angiogenic-mediated

PT diseases
 XX
 XX Claim 5; Page 99-100; 121pp; English.
 XX
 CC The specification describes multifunctional proteins which comprise
 CC combinations of angiostatin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have
 CC anti-angiogenic and/or anti-tumor activity. The multifunctional protein
 CC may exhibit useful properties such as having similar or greater
 CC biological activity when compared to a single factor or by having
 CC improved half-life or decreased adverse side effects, or a combination
 CC of these properties. The proteins can be used for treating an
 CC angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular
 CC degeneration, or arthritis. They can also be used for inhibiting the
 CC production of tumor cells (characteristic of lung, breast, ovarian,
 CC prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma,
 CC hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor
 CC growth. The present sequence represents a multifunctional protein of the
 CC invention.
 CC
 SQ Sequence 297 AA;
 Query Match 78.5%; Score 423; DB 20; Length 297;
 Best Local Similarity 78.7%; Pred. No. 2,4e-31;
 Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 2 SPVVDGCHGDSRGYSSTVTGRTCCSSSMIPHHORTPENYPNAGLTENYCRNP 61
 DB 209 TPVVDGCHGDSRGYSSTVTGRTCCSSSMIPHHOKTBNYPNAGLTENYCRNP 268
 QY 62 SGKQPMCYTTPCVRWEYCNLTQCSETES 90
 DB 269 ADKGPWCFTTDPVRWEYCNLTQKCSGTEA 297
 Db
 RESULT 6
 AAY08687
 ID AAY08687 standard; Protein; 361 AA.
 XX
 AC AAY08687;
 XX
 DT 10-AUG-1999 (first entry)
 XX
 DE Human angiostatin protein fragment.
 XX
 KW Plasmidogen; human; angiostatin; endostatin; gene therapy; vector;
 KW anti-angiogenic; attenuation; cytosol; anti-diabetic; ophthalmology;
 KW tumour growth; solid tumour; diabetic retinopathy; retina.
 XX
 OS Homo sapiens.
 XX
 PN WO9226480-A1.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-US24950.
 XX
 PR 20-NOV-1997; 97US-0975424.
 XX
 PA (GENE-) GENETIX PHARM INC.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Bachelot T, Leboulch P, Pawliuk Rd;
 XX
 DR WPI, 1999-357696/30.
 DR N-PSDB; AAX77713.
 XX
 PT Anti-angiogenic gene therapy vectors
 XX
 PS Disclosure; Page 59-60; 83pp; English.
 CC
 CC This invention describes a novel viral gene therapy vector comprising a
 CC nucleic acid molecule encoding an anti-angiogenic polypeptide chosen

CC from human or murine angiostatin, human or murine endostatin and
 CC angiogenesis-inhibiting fusions and fragments, where the viral vector is
 CC sufficiently attenuated for use in human gene therapy. The products of
 CC the invention have anti-angiogenic, cytosolic, anti-diabetic and
 CC ophthalmological activity. The vector is used in gene therapy for
 CC inhibiting tumour growth in humans harbouring a solid tumour. The vector
 CC expresses an anti-angiogenic polypeptide. An additional use comprises
 CC treatment of diabetic retinopathy, where the anti-angiogenic polypeptide
 CC inhibits angiogenesis in the vicinity of the retina. The vector is
 CC administered to cells ex vivo and then administered to the patient.
 CC
 SQ Sequence 361 AA;
 Query Match 78.5%; Score 423; DB 20; Length 361;
 Best Local Similarity 78.7%; Pred. No. 3e-31;
 Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 2 SPVVDGCHGDSRGYSSTVTGRTCCSSSMIPHHORTPENYPNAGLTENYCRNP 61
 DB 273 TPVVDGCHGDSRGYSSTVTGRTCCSSSMIPHHOKTBNYPNAGLTENYCRNP 332
 QY 62 SGKQPMCYTTPCVRWEYCNLTQCSETES 90
 DB 333 ADKGPWCFTTDPVRWEYCNLTQKCSGTEA 361
 Db
 RESULT 7
 AAY70255
 ID AAY70255 standard; Protein; 363 AA.
 XX
 AC AAY70255;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Human angiogenesis inhibitor, angiostatin.
 XX
 KW Human; immunoglobulin gamma Fc fragment; angiostatin; immunofusion;
 KW angiogenesis; inhibitor; cytosolic; antirheumatoid; antiarthritic;
 KW antiproliferative; antidiabetic; ophthalmological; immunosuppressant;
 KW vasotropic; vulnery; treatment; antiarteriosclerosis; tumour;
 KW metastasis; atherosclerosis; psoriasis; rheumatoid arthritis;
 KW ocular angiogenic disease; diabetic retinopathy; macular degeneration;
 KW myocardial angiogenesis; plaque neovascularization; telangiectasia;
 KW wound granulation; keloid scar; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200011033-A2.
 XX
 PD 02-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-US19329.
 XX
 PR 25-AUG-1998; 98US-0097883.
 XX
 PA (LEXI-) LEXINGEN PHARM CORP.
 XX
 PI Lo K, Li Y, Gillies SD;
 XX
 DR WPI, 2000-237616/20.
 DR N-PSDB; AAZ51295.
 XX
 PT Novel fusion protein of angiostatin or endostatin and an immunoglobulin
 PT Fc region, useful for treating conditions mediated by angiogenesis -
 PT such as rheumatoid arthritis, tumors and macular degeneration -
 XX
 PS Example 4; Pages 45-46; 68pp; English.
 CC
 CC The patent discloses a DNA molecule encoding a fusion protein comprising
 CC a signal sequence, an immunoglobulin Fc region, and an angiogenesis
 CC inhibitor selected from angiostatin, endostatin, a plasmidogen fragment
 CC having angiostatin activity, a collagen XVIII fragment having endostatin
 CC activity, or combinations of them. The fusion protein (immunofusion) is

CC used to inhibit angiogenesis and to treat diseases or conditions mediated
 CC by angiogenesis. Conditions that may be treated include solid tumours,
 CC blood born tumours, tumour metastasis, benign tumours including
 CC haemangiomas, acoustic neuromas, neurofibromas, trichomas and pyrogenic
 CC granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases
 CC e.g. diabetic retinopathy, retinopathy of prematurity, macular
 CC degeneration, corneal graft rejection, neovascular glaucoma, retrolental
 CC fibroplasia, rubeosis and Oeler-Weber syndrome; myocardial angiogenesis,
 CC plaque neovascularisation, telangiectasia, haemophilic joints,
 CC angiodysplasia, wound granulation, and excessive or abnormal stimulation of
 CC endothelial cells, intestinal cells, atherosclerosis, sclerodermal and
 CC hypertrophic scars, i.e. keloid scars. The DNA constructs may be used
 CC in gene therapy. The present sequence is a human
 CC angiotensin used in the construction of immunofusion containing human
 CC immunoglobulin gamma (IgG) Fc fragment.

XX Sequence 363 AA;

Query Match 78.5%; Score 423; DB 21; Length 363;

Best Local Similarity 78.7%; Pred. No. 3e-31; Mismatches 11; Indels 0; Gaps 0;

Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCHGDRGSRGISTTVTGRTQSWSSMIPMHQRTPEPNYPAGLTENTYCRND 61

DB 275 TPVQDCHGDRGSRGISTTVTGRTQSWSSMIPMHQRTPEPNYPAGLTENTYCRND 334

QY 62 SGKQPCWCTTDPCEWMEYCNLTQCSSTES 90

DB 335 ADKGPWCFTTDPCEWMEYCNLTQCSSTES 363

RESULT 8

ID AAY02106 standard; Protein, 364 AA.

AC AAY02106;

DT 16-JUL-1999 (first entry)

DE A multifunctional protein of the invention.

KW Angiostatin; endostatin; interferon; thrombospondin;

KW anti-tumor; multifunctional protein; platelet factor 4; anti-angiogenic;

KW cancer; diabetic retinopathy; macular degeneration; arthritis;

KW tumor cell production.

OS Synthetic.

OS Homo sapiens.

PN WO9916889-A1.

PD 08-APR-1999.

PF 30-SEP-1998; 98WO-US20464.

PR 01-OCT-1997; 97US-0060609.

PA (SEAR) SEARLE & CO G D.

PI Bolanowski MA, Caparon MH, Caspersen GF, Gregory SA,

DR Klein BK, McKearn UP;

XX WPI, 1999-255098/21.

XX New multifunctional proteins useful for treating angiogenic-mediated

XX diseases

XX Claim 5; Page 101-102; 121pp; English.

XX The specification describes multifunctional proteins which comprise

XX combinations of angiostatin, endostatin, interferon, thrombospondin,

CC anti-angiogenic and/or anti-tumor activity. The multifunctional protein
 CC may exhibit useful properties such as having similar or greater
 CC biological activity when compared to a single factor or by having
 CC improved half-life or decreased adverse side effects, or a combination
 CC of these properties. The proteins can be used for treating an
 CC angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular
 CC degeneration, or arthritis. They can also be used for inhibiting the
 CC production of tumor cells (characteristic of lung, breast, ovarian,
 CC prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma,
 CC hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor
 CC growth. The present sequence represents a multifunctional protein of the
 CC invention.

XX Sequence 364 AA;

Query Match 78.5%; Score 423; DB 20; Length 364;

Best Local Similarity 78.7%; Pred. No. 3e-31; Mismatches 11; Indels 0; Gaps 0;

Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCHGDRGSRGISTTVTGRTQSWSSMIPMHQRTPEPNYPAGLTENTYCRND 61

DB 276 TPVQDCHGDRGSRGISTTVTGRTQSWSSMIPMHQRTPEPNYPAGLTENTYCRND 335

QY 62 SGKQPCWCTTDPCEWMEYCNLTQCSSTES 90

DB 336 ADKGPWCFTTDPCEWMEYCNLTQCSSTES 364

RESULT 9

ID AAB01905 standard; Protein, 364 AA.

AC AAB01905;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringles 1-4 (angiostatin).

KW Plasminogen; human; kringles domain; endothelial cell proliferation;

KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;

KW antiproliferative; antiinflammatory; antitumor; antineoplastic; antiarthritic;

KW antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

OS US6057122-A.

PN 02-MAY-2000.

PD 05-MAY-1997; 97US-0851350.

PF 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

PA (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI, 2000-349573/30.

XX Preparation of Kringles five peptide fragment for treating various

XX disorders such as angiogenic, ocular, skin diseases and cancer,

XX involves mixing mammalian plasminogen and elastase followed by

XX incubation and isolation -

XX Example 17; Page -; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringles 5

XX and peptide fragments. The method comprises mixing mammalian plasminogen and

CC and carcinomas of various organs such as breast, genital tract,
CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
CC arising from haematopoietic malignancies such as leukemias and
CC lymphomas. They are also used for the prophylaxis of various autoimmune
CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
CC (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Weber
CC syndrome), diseases caused by excessive or abnormal stimulation of
CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
CC disease and ulcers). The peptides are also useful as a birth control
CC agent which inhibits ovulation and establishment of the placenta.
CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
CC in an exemplification of the invention.
CC Note: This sequence is not shown in the specification, but is derived
CC from the full length human plasminogen sequence (AAB01887) shown in
CC figure 1.

SQ Sequence 364 AA;

Query Match 78.5%; Score 423; DB 21; Length 364;
Best Local Similarity 78.7%; Pred. No. 3e-31;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDQCYHGDGRSYRGISSTVTGRTQSSSMIPHHQRTPEYPNAGLTENYCRND 61
DB 273 TPVVDQCYHGDQSYRGISSTVTGRTQSSSMTPHHQKTPENYPNAGLTENYCRND 332
QY 62 SGKQPMWCYTTDPCVRWEYCNLTQCSSTES 90
DB 333 ADKGPMCFITDPSVRWEYCNLKKCSGTEA 361

RESULT 10

ID AAY53868 standard; protein; 369 AA.

AC AAY53868;

DT 13-MAR-2000 (first entry)

DE Amino acid sequence of human angiotensin protein.

XX Human; plasminogen; angiotensin; greenstatin; thrombolytic factor;
XX angiotensin inhibitory protein; proliferation; angiogenesis; cancer;
XX vascular endothelial cell; ophthalmic disease; glaucoma;
XX diabetic retinopathy; arthritis; psoriasis.

OS Homo sapiens.

PN MO9961464-A1.

PD 02-DEC-1999.

PF 28-MAY-1999; 99WO-KR00263.

PR 28-MAY-1998; 98KR-0019535.

PR 27-MAY-1999; 99KR-0019144.

PA (GREG) KOREA GREEN CROSS CORP.

XX You WK, So SH, Ahn BC, Lee H, Jung S, Kim Y, Lee JH, Hong Y,
XX Joe YA, Chang S,
XX WPI; 2000-086703/07.

XX Purifying angiogenesis inhibitors produced as recombinant proteins in
XX Escherichia coli, useful as anticancer agents and for treating ocular
XX diseases -

PS Claim 2, Page 45-47; 55pp; English.

XX The present sequence represents the human angiotensin protein. It
XX is derived from the plasminogen protein, and comprises amino acids

CC 99-467. Greenstatin is also derived from plasminogen, and comprises
CC amino acids 101-354. Angiotensin and greenstatin are used as
CC thrombolytic factors and angiogenesis inhibitory proteins. Angiotensin
CC contains the kringles 1-4 region of plasminogen, and greenstatin contains
CC the kringles 1-3 region of plasminogen. As both proteins contain a high
CC number of disulphide bonds, they are difficult to purify. The
CC specification describes a method for the purification of such
CC angiogenesis inhibitory proteins. The method comprises solubilising
CC the proteins, produced as inclusion bodies in Escherichia coli and
CC refolding the solubilised fraction in buffer containing urea and
CC glutathione. The angiogenesis inhibitory proteins specifically inhibit
CC proliferation of vascular endothelial cells, but not that of
CC non-endothelial cancers or normal cells. The angiogenesis inhibitory
CC proteins are used to suppress angiogenesis, specifically for treating
CC cancers (e.g. of lung, skin and brain) or ophthalmic diseases (e.g.
CC glaucoma and diabetic retinopathy), but also arthritis and psoriasis.

SQ Sequence 369 AA;

Query Match 78.5%; Score 423; DB 21; Length 369;
Best Local Similarity 78.7%; Pred. No. 3e-31;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDQCYHGDGRSYRGISSTVTGRTQSSSMIPHHQRTPEYPNAGLTENYCRND 61
DB 273 TPVVDQCYHGDQSYRGISSTVTGRTQSSSMTPHHQKTPENYPNAGLTENYCRND 332
QY 62 SGKQPMWCYTTDPCVRWEYCNLTQCSSTES 90
DB 333 ADKGPMCFITDPSVRWEYCNLKKCSGTEA 361

RESULT 11

ID AAY79226 standard; protein; 374 AA.

AC AAY79226;

DT 19-JUN-2000 (first entry)

DE Angiotensin inhibitor obtained by plasminogen cleavage.

XX Angiotensin inhibitor; plasminogen; human; K4 protease;
XX snake venom; cobra; antimetastatic; cytostatic; antitumour; tumour;
XX prostate cancer; breast cancer; colon cancer; lung cancer;
XX leukemia; metastasis; contraceptive; therapy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Modified-site 264 /note- "N-glycosylated"

PN MO200010506-A2.

PD 02-MAR-2000.

PF 19-AUG-1999; 99WO-US18877.

PR 20-AUG-1998; 98US-0097244.

PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

PI Mann KG, Jenny NS;

XX WPI; 2000-246485/21.

XX New angiogenesis inhibitors useful for treating solid tumors,
XX leukemias, tumor metastasis, benign tumor, rheumatoid arthritis,
XX psoriasis and ocular angiogenic diseases -

PS Claim 1, Fig 10; 72pp; English.

CC The present sequence represents a preferred angiogenesis inhibitor
 CC of the invention that is obtained by cleavage of human plasminogen
 CC with splitting cobra (Naja nigricollis nigricollis) venom K4
 CC protease and plasmin. The K4 protease cleaves native plasminogen
 CC following amino acid residue 452, with little or no disruption of
 CC the first 4 plasminogen kringles. Plasmin cleaves between residues
 CC 77 and 78 of human plasminogen. Thus, the present protein spans
 CC amino acid residues 78-451 of plasminogen. The angiogenesis
 CC inhibitors obtained from plasminogen can be used to inhibit tumour
 CC growth in a mammal, preferably human. They are useful for treating
 CC angiogenesis-associated diseases such as: solid tumours, prostate
 CC cancer, breast cancer, colon cancer and lung cancer (claimed);
 CC blood-borne tumors such as leukaemia; metastasis; benign tumours;
 CC rheumatoid arthritis; psoriasis; ocular angiogenic diseases;
 CC myocardial angiogenesis; plaque neovascularization; telangiectasia;
 CC haemophilic joints; angiodioma; wound granulation; excessive or
 CC abnormal stimulation of endothelial cells; and as birth control
 CC agents by preventing vascularization required for embryo
 CC implantation. The inhibitors are administered also to extend the
 CC dormancy of micrometastases and to stabilize any residual primary
 CC tumour.

XX Sequence 374 AA;

Query Match 78.5%; Score 423; DB 21; Length 374;
 Best Local Similarity 78.7%; Pred. No. 3.1e-31;
 Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDRGSRGISTTGTTCQSSSMTHHQRTPENYPNAGLTENTCRND 61

DB 274 TPVVDCHGDRGSGSYRGTSSTTTGKCKQSSSMTPHRHQKTPENYPNAGLTMYCRND 333

QY 62 SGKQPCYTTDPCVRWEYCNLTQCES 90

DB 334 ADKGPWCFTTDPSSVRWEYCNLKKGCGTEA 362

RESULT 12

AAV79225

ID AAV79225 standard; Protein; 375 AA.

XX AAV79225;

DT 19-JUN-2000 (first entry)

XX Angiogenesis inhibitor obtained by plasminogen cleavage.

XX Angiogenesis inhibitor; plasminogen; human; K4 protease;

KW snake venom; cobra; antimetastatic; cytosstatic; antitumour; tumour;

KW prostate cancer; breast cancer; colon cancer; lung cancer;

KW leukaemia; metastasis; contraceptive; therapy.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

PH Modified-site 265 /note- "N-glycosylated"

FT WO200010506-A2.

XX 02-MAR-2000.

PD 19-AUG-1999; 99WO-US18877.

XX 20-AUG-1998; 98US-0097244.

XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

XX Mann KG, Jenny NS;

XX WPI; 2000-246485/21.

XX New angiogenesis inhibitors useful for treating solid tumors,

PT leukemias, tumor metastasis, benign tumor, rheumatoid arthritis,
 PR psoriasis and ocular angiogenic diseases -
 XX Claim 1; Fig 9; 72pp: English.

CC The present sequence represents a preferred angiogenesis inhibitor
 CC of the invention that is obtained by cleavage of human plasminogen
 CC with splitting cobra (Naja nigricollis nigricollis) venom K4
 CC protease and plasmin. The K4 protease cleaves native plasminogen
 CC following amino acid residue 452, with little or no disruption of
 CC the first 4 plasminogen kringles. Plasmin cleaves between residues
 CC 77 and 78 of human plasminogen. Thus, the present protein spans
 CC amino acid residues 77-451 of plasminogen. The angiogenesis
 CC inhibitors obtained from plasminogen can be used to inhibit tumour
 CC growth in a mammal, preferably human. They are useful for treating
 CC angiogenesis-associated diseases such as: solid tumours, prostate
 CC cancer, breast cancer, colon cancer and lung cancer (claimed);
 CC blood-borne tumors such as leukaemia; metastasis; benign tumours;
 CC rheumatoid arthritis; psoriasis; ocular angiogenic diseases;
 CC myocardial angiogenesis; plaque neovascularization; telangiectasia;
 CC haemophilic joints; angiodioma; wound granulation; excessive or
 CC abnormal stimulation of endothelial cells; and as birth control
 CC agents by preventing vascularization required for embryo
 CC implantation. The inhibitors are administered also to extend the
 CC dormancy of micrometastases and to stabilize any residual primary
 CC tumour.

XX Sequence 375 AA;

Query Match 78.5%; Score 423; DB 21; Length 375;
 Best Local Similarity 78.7%; Pred. No. 3.1e-31;
 Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDRGSRGISTTGTTCQSSSMTHHQRTPENYPNAGLTENTCRND 61

DB 275 TPVVDCHGDRGSGSYRGTSSTTTGKCKQSSSMTPHRHQKTPENYPNAGLTMYCRND 334

QY 62 SGKQPCYTTDPCVRWEYCNLTQCES 90

DB 335 ADKGPWCFTTDPSSVRWEYCNLKKGCGTEA 363

RESULT 13

AAW07579

ID AAW07579 standard; Protein; 378 AA.

XX AAW07579;

DT 22-JUN-1997 (first entry)

XX Human kringles 1-4BKLS.

XX angiotatin; plasminogen; kringles; angiogenesis; cancer; arthritis;

KW macular degeneration; diabetic retinopathy.

XX Homo sapiens.

OS Homo sapiens.

XX WO9635774-A2.

XX 14-NOV-1996.

PD 26-APR-1996; 96WO-US05856.

XX 08-MAR-1996; 96US-0612788.

XX 26-APR-1995; 95US-0429743.

XX 22-FEB-1996; 96US-0605598.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;

XX WPI; 1996-518662/51.

PT Use of angiotensin fragments or aggregates - for inhibiting
PT endothelial cell proliferation and treating angiotensin-mediated
PT diseases, e.g. cancer, arthritis or diabetic retinopathy

PS Claim 4; Page 140-141; 203pp; English.

CC The invention relates to new methods and compositions for
CC inhibiting endothelial cell proliferation, using as active component
CC an angiotensin fragment, a combination of angiotensin fragments, or
CC aggregate angiotensin. The fragment is preferably derived from murine,
CC human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
CC kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle
CC 1-4 or kringle 1-4BKS protein. The aggregate angiotensin has a Mol. wt.
CC of 45-65 kD and is derived from a plasminogen fragment beginning at
CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
CC bovine plasminogen. The active component can be used for treating
CC angiotensin-mediated diseases such as cancer, arthritis, macular
CC degeneration and diabetic retinopathy. It can also be used to develop
CC antibodies for use in diagnosis, detection and therapy.
CC The present sequence, human kringle 1-4BKS, is a specific angiotensin
CC fragment which can be used in the invention.

CC Sequence 378 AA;

Query Match 78.5%; Score 423; DB 17; Length 378;

Best Local Similarity 78.7%; Pred. No. 3.1e-31; Mismatches 11; Indels 0; Gaps 0;

Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNAGLTENYCRND 61

DB 279 TPVVDCCYHGDGQSYRGISSTTTTGKCSWSSMTPHRRQKTPENYPNAGLTENYCRND 338

QY 62 SGKQPCYTTDPCVMEYCNLTQCSSTES 90

DB 339 ADKGPWCFTTDPSEVMEYCNLTQCSSTEA 367

RESULT 14

AAB16450 standard; Protein; 378 AA.

AC AAB16450;

DT 27-OCT-2000 (first entry)

DE Human angiotensin protein sequence.

XX Angiotensin-inhibiting protein receptor; angiotensin;
XX endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
XX psoriasis; scleroderma; myocardial angiotensin; Crohn's disease;
XX cerebral collateral; arteriovenous malformation; rheumatoid arthritis; cancer;
XX diabetic retinopathy; arthritis; wound healing; peptic ulcer;
XX Helicobacter related disease; fracture; cat scratch fever.

OS Homo sapiens.

PN WO200032631-A2.

PD 08-JUN-2000.

PF 06-DEC-1999; 99MO-US28897.

PR 04-DEC-1998; 98US-0206059.

PA (ENTR-) ENTREMED INC.

PI MacDonald NJ, Sim KL;

DR WPI; 2000-412290/35.

PT New angiotensin-inhibiting protein receptors, useful in methods for
PT treating diseases and processes that are mediated by angiotensin, such
PT as solid tumours, psoriasis, scleroderma and myocardial angiotensin -

XX Disclosure, Figure 2, 100pp; English.

CC This invention relates to angiotensin-inhibiting protein receptors, and
CC the DNA sequences encoding them. Angiotensin is the generation of new
CC blood vessels into a tissue, and normally occurs in wound healing,
CC foetal and embryonal development and the formation of the corpus luteum,
CC endometrium and placenta. Angiotensin is a protein (see AAB16450 and
CC AAB68202) involved in angiotensin, and has an amino acid sequence
CC similar to that of a plasminogen fragment (see murine plasminogen
CC AAB16490). Angiotensin has the ability to inhibit angiotensin.

CC Endostatin is also an angiotensin inhibiting protein (see AAB16451 and
CC AAB68203). Sequences AAB68242 and AAB16522 represent coding and protein
CC sequences of human laminin. Laminin is an angiotensin binding protein,
CC and some of the peptides of the invention share homology with regions of
CC laminin. Peptides AAB16452-816521 (excluding AAB16490) are the
CC angiotensin-inhibiting protein receptor fragments of the invention. The
CC peptides bind either angiotensin or endostatin and can be used in methods
CC for treating diseases and processes that are mediated by angiotensin,
CC such as solid tumours, psoriasis, scleroderma, myocardial angiotensin,
CC Crohn's disease, cerebral collateral, arteriovenous malformations,
CC rheumatoid arthritis, wound healing, peptic ulcers,
CC Helicobacter related diseases, fractures, placental and cat scratch
CC fever. They are useful for the detection and prognosis of cancer. DNA
CC sequences A628204-A628241 encode the peptides of the invention.

CC Sequence 378 AA;

Query Match 78.5%; Score 423; DB 21; Length 378;

Best Local Similarity 78.7%; Pred. No. 3.1e-31; Mismatches 11; Indels 0; Gaps 0;

Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNAGLTENYCRND 61

DB 279 TPVVDCCYHGDGQSYRGISSTTTTGKCSWSSMTPHRRQKTPENYPNAGLTENYCRND 338

QY 62 SGKQPCYTTDPCVMEYCNLTQCSSTES 90

DB 339 ADKGPWCFTTDPSEVMEYCNLTQCSSTEA 367

RESULT 15

AAM48894 standard; Protein; 378 AA.

AC AAM48894;

DT 04-APR-2002 (first entry)

DE Human angiotensin protein.

XX Human; angiotensin; endostatin; angiotensin; cancer; metastasis;
XX psoriasis; scleroderma; Crohn's disease; corneal disease;
XX retinopathy; arthritis; wound healing; Helicobacter pylori; peptic ulcer;
XX gene therapy; angiotensin antagonist; endostatin antagonist;
XX antiangiogenic; cytoabatic; antiarthritic; antiinflammatory;
XX cerebroprotective; antidiabetic; vitamin; antipyretic; vulnerary;
XX gynaecological; cat scratch fever.

OS Homo sapiens.

PN WO200193897-A2.

PD 13-DEC-2001.

PF 04-JUN-2001; 2001MO-US17947.

PR 02-JUN-2000; 2000US-209065P.

PR 08-MAY-2001; 2001US-289387P.

PA (ENTR-) ENTREMED INC.

PI Sim KL, MacDonald NJ;

XX WPI, 2002-130569/17.

DR
XX
PT Regulating angiogenesis and treatment of angiogenesis-mediated
PT diseases, e.g. hemangioma, tumors or cancer, by administering a
PT tropomyosin binding compound or actin disrupting compound -
XX

PS Disclosure, Fig 2; 95pp; English.

XX
XX
CC The present invention relates to methods of regulating angiogenesis in an
CC individual by administering an angiogenesis regulating composition
CC comprising a tropomyosin binding compound or an actin disrupting
CC compound. The compositions are useful for treating diseases and processes
CC mediated by angiogenesis including haemangioma, solid tumours, blood
CC borne tumours, leukaemia, metastasis, Crohn's disease, coronary or
CC cerebral collaterals, arthritis, diabetic neovascularisation, macular
CC degeneration, wound healing, Helicobacter related diseases, ovulation,
CC menstruation, and cat scratch fever. The present sequence is a protein
CC described in the exemplification of the invention.
XX

SQ Sequence 378 AA;

Query Match 78.5%; Score 423; DB 23; Length 378;
Best Local Similarity 78.7%; Pred. No. 3.1e-31;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVDDCYHGDGRSYRGISSTVTGRTGCSWSSMI PHMHQRTPNYPNAGLTENYCRNPD 61
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
279 TPVDDCYHGDGRSYRGISSTVTGRTGCSWSSMTPHRHOKTPENPNAGLTENYCRNPD 338
QY 62 SGKOPWCYTTDPCVWMEYCNLTQCSSETS 90
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
339 ADKGPWCFTTDBSVWMEYCNLTQCSSETS 367

Search completed: January 12, 2004, 17:23:21
Job time : 37.2632 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 17:24:03 ; Search time 26.6842 Seconds
(without alignments)
687.200 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539
Sequence: 1 KSPVVQDCYHGDGRSYRGIS.....DPCVWEYCNLTQCSFESG 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_Aa.*
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16: /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	539	100.0	1169	10	US-09-870-759-126
2	539	100.0	1169	12	US-09-751-708A-126
3	430	79.8	368	9	US-09-761-120-42
4	430	79.8	368	12	US-10-402-364-42
5	423	78.5	363	12	US-10-292-418-11
6	423	78.5	378	9	US-09-873-676-1
7	423	78.5	378	10	US-09-335-325-42
8	423	78.5	391	15	US-10-131-241-42
9	423	78.5	394	15	US-10-304-287-7
10	423	78.5	394	15	US-10-304-287-8
11	423	78.5	458	9	US-09-846-893-4
12	423	78.5	569	9	US-09-846-893-5
13	423	78.5	571	9	US-09-846-893-8
14	423	78.5	576	9	US-09-846-893-6
15	423	78.5	791	10	US-09-967-386-1

16	423	78.5	791	15	US-10-304-287-1	Sequence 1, Appli
17	423	78.5	810	9	US-09-946-893-2	Sequence 2, Appli
18	423	78.5	810	12	US-10-237-144-1	Sequence 1, Appli
19	423	78.5	810	15	US-10-193-656-2	Sequence 2, Appli
20	410	76.1	352	9	US-09-761-120-40	Sequence 40, Appli
21	410	76.1	352	9	US-09-335-325-40	Sequence 40, Appli
22	410	76.1	352	12	US-10-402-364-40	Sequence 40, Appli
23	410	76.1	352	15	US-10-131-241-40	Sequence 40, Appli
24	397	73.7	364	15	US-10-157-369-4	Sequence 4, Appli
25	397	73.7	451	15	US-10-157-369-2	Sequence 2, Appli
26	392	72.7	359	12	US-10-292-418-40	Sequence 40, Appli
27	388	72.0	362	12	US-10-292-418-25	Sequence 25, Appli
28	388	72.0	378	9	US-09-761-120-41	Sequence 41, Appli
29	388	72.0	378	10	US-09-335-325-41	Sequence 41, Appli
30	388	72.0	378	12	US-10-402-364-41	Sequence 41, Appli
31	388	72.0	378	15	US-10-131-241-41	Sequence 41, Appli
32	388	72.0	459	9	US-09-761-120-46	Sequence 46, Appli
33	388	72.0	459	12	US-10-402-364-46	Sequence 46, Appli
34	388	72.0	812	9	US-09-788-142-1	Sequence 1, Appli
35	388	72.0	812	9	US-09-761-120-1	Sequence 1, Appli
36	388	72.0	812	9	US-09-873-676-81	Sequence 81, Appli
37	388	72.0	812	10	US-09-335-325-1	Sequence 1, Appli
38	388	72.0	812	12	US-10-402-364-1	Sequence 1, Appli
39	388	72.0	812	15	US-10-131-241-1	Sequence 1, Appli
40	383	71.1	78	9	US-09-753-064-5	Sequence 5, Appli
41	383	71.1	78	9	US-09-761-120-23	Sequence 23, Appli
42	383	71.1	78	10	US-09-335-325-23	Sequence 23, Appli
43	383	71.1	78	12	US-10-267-137-9	Sequence 9, Appli
44	383	71.1	78	12	US-10-402-364-23	Sequence 23, Appli
45	383	71.1	78	12	US-10-402-364-52	Sequence 52, Appli

ALIGNMENTS

RESULT 1
US-09-870-759-126
; Sequence 126, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-126

Query Match 100.0%; Score 539; DB 10; Length 1169;
Best Local Similarity 100.0%; Pred. No. 1,1e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSPVVQDCYHGDGRSYRGISSTVTGTCQSSMIMPHQRTPEPNAGITENYCNP 60
DB 624 KSPVVQDCYHGDGRSYRGISSTVTGTCQSSMIMPHQRTPEPNAGITENYCNP 683
QY 61 DSGKOPWCYTTDPCVWEYCNLTQCSFESG 91
DB 684 DSGKOPWCYTTDPCVWEYCNLTQCSFESG 714

RESULT 2
US-09-751-708A-126
; Sequence 126, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:

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; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751108
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-751-708A-126

Query Match          100.0%; Score 539; DB 12; Length 1169;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 KSPVQDCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNYPNAGLTENYCRNP 60
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QY 61 DSGKQPCYTTDPCVRMEYCNLTQCSSETS 91
684 DSGKQPCYTTDPCVRMEYCNLTQCSSETS 714
Db

RESULT 3
US-09-761-120-42
; Sequence 42, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05940-0151 (43171-252068)
; CURRENT APPLICATION NUMBER: US/09/761,120
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Kringle 1-4 BKLS
; US-09-761-120-42

Query Match          79.8%; Score 430; DB 9; Length 368;
Best Local Similarity 79.8%; Pred. No. 2e-38;
Matches 71; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNYPNAGLTENYCRNP 61
Db 269 TPVQDCYHGDGRSYRGISSTVTGRTCSWSSMTPHROKTPENYPNAGLTENYCRNP 328
QY 62 SGKQPCYTTDPCVRMEYCNLTQCSSETS 90
Db 329 ADKQPCYTTDPCVRMEYCNLTQCSSETS 357

RESULT 4
US-10-402-364-42
; Sequence 42, Application US/10402364
; Publication No. US20040002455A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael
; US-10-402-364-42
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; APPLICANT: Folkman, M. Judah
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05213-2151 (43170-252068)
; CURRENT APPLICATION NUMBER: US/10/402,364
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/761,120A
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Kringle 1-4 BKLS
; US-10-402-364-42

Query Match          79.8%; Score 430; DB 12; Length 368;
Best Local Similarity 79.8%; Pred. No. 2e-38;
Matches 71; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNYPNAGLTENYCRNP 61
Db 269 TPVQDCYHGDGRSYRGISSTVTGRTCSWSSMTPHROKTPENYPNAGLTENYCRNP 328
QY 62 SGKQPCYTTDPCVRMEYCNLTQCSSETS 90
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RESULT 5
US-10-292-418-11
; Sequence 11, Application US/10292418
; Publication No. US20030139365A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Li, Yue
; APPLICANT: Gillies, Stephen D
; TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
; FILE REFERENCE: LEX-006C1
; CURRENT APPLICATION NUMBER: US/10/292,418
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/383,315
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 60/097,883
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-418-11

Query Match          78.5%; Score 423; DB 12; Length 363;
Best Local Similarity 78.7%; Pred. No. 1.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNYPNAGLTENYCRNP 61
Db 275 TPVQDCYHGDGRSYRGISSTVTGRTCSWSSMTPHROKTPENYPNAGLTENYCRNP 334
QY 62 SGKQPCYTTDPCVRMEYCNLTQCSSETS 90
Db 335 ADKQPCYTTDPCVRMEYCNLTQCSSETS 363
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RESULT 6
US-09-873-676-1
; Sequence 1, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-676-1
Query Match 78.5%; Score 423; DB 9; Length 378;
Best Local Similarity 78.7%; Pred. No. 1.2e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 2 SPVVDCTCHGDRGSRIGISSTTVTGRTCSWSMTPHMQRTPEPNYPNAGLTENYCRNP 61
DB 279 TPVVDCTCHGDRGSRIGISSTTVTGRTCSWSMTPHMQRTPEPNYPNAGLTENYCRNP 338
QY 62 SGKOPWCYTTDPCVRWEYCNLTQCSSETS 90
DB 339 ADKGPWCFTTDPVSVMWEYCNLKKGSGTEA 367
RESULT 7
US-09-335-325-42
; Sequence 42, Application US/09335325
; Patent No. US20020164717A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; Cao, Yihai
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/335,325
; FILING DATE: 17-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,788
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; REFERENCE/DOCKET NUMBER: 05213-0126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: KL-4BKLS
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-335-325-42
Query Match 78.5%; Score 423; DB 10; Length 378;
Best Local Similarity 78.7%; Pred. No. 1.2e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 2 SPVVDCTCHGDRGSRIGISSTTVTGRTCSWSMTPHMQRTPEPNYPNAGLTENYCRNP 61
DB 279 TPVVDCTCHGDRGSRIGISSTTVTGRTCSWSMTPHMQRTPEPNYPNAGLTENYCRNP 338
QY 62 SGKOPWCYTTDPCVRWEYCNLTQCSSETS 90
DB 339 ADKGPWCFTTDPVSVMWEYCNLKKGSGTEA 367
RESULT 8
US-10-131-241-42
; Sequence 42, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
; APPLICANT: Holaday, John W.
; APPLICANT: Fortier, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
; FILE REFERENCE: 05213-0344 43170-271565
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/10/131,241
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/086,586
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-241-42
Query Match 78.5%; Score 423; DB 15; Length 378;
Best Local Similarity 78.7%; Pred. No. 1.2e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
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DB 279 TPVVDCTCHGDRGSRIGISSTTVTGRTCSWSMTPHMQRTPEPNYPNAGLTENYCRNP 338
QY 62 SGKOPWCYTTDPCVRWEYCNLTQCSSETS 90
DB 339 ADKGPWCFTTDPVSVMWEYCNLKKGSGTEA 367
RESULT 9
US-10-304-287-7
; Sequence 7, Application US/10304287
; Publication No. US20030083234A1

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/ GENERAL INFORMATION:
/ APPLICANT: Waisman, David M.
/ APPLICANT: Kwon, MiJung
/ TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
/ FILE REFERENCE: ME02-001
/ CURRENT APPLICATION NUMBER: US/10/304,287
/ CURRENT FILING DATE: 2002-11-26
/ PRIOR APPLICATION NUMBER: US 60/333,866
/ PRIOR FILING DATE: 2001-11-28
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Microsoft Word
/ SEQ ID NO 7
/ LENGTH: 391
/ TYPE: PRT
/ ORGANISM: mammalian
US-10-304-287-7

Query Match      78.5%; Score 423; DB 15; Length 391;
Best Local Similarity 78.7%; Pred. No. 1.2e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

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DB      275 TPVQDCYHGDGSRYSIGISSTVTGRTCCSSMIPHHORTPENYPNAGLTENYCRNP 334
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QY      62 SGKQPCYTTDPCVRWEYCNLTQCSSETS 90
DB      335 ADKGPWCFTTDPBVRWEYCNLKKCSGTEA 363
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-10-304-287-8
/ Sequence 8, Application US/10304287
/ Publication No. US20030083234A1
/ GENERAL INFORMATION:
/ APPLICANT: Waisman, David M.
/ APPLICANT: Kwon, MiJung
/ TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
/ FILE REFERENCE: ME02-001
/ CURRENT APPLICATION NUMBER: US/10/304,287
/ CURRENT FILING DATE: 2002-11-26
/ PRIOR APPLICATION NUMBER: US 60/333,866
/ PRIOR FILING DATE: 2001-11-28
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Microsoft Word
/ SEQ ID NO 8
/ LENGTH: 394
/ TYPE: PRT
/ ORGANISM: mammalian
US-10-304-287-8

Query Match      78.5%; Score 423; DB 15; Length 394;
Best Local Similarity 78.7%; Pred. No. 1.3e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY      2 SPVQDCYHGDGSRYSIGISSTVTGRTCCSSMIPHHORTPENYPNAGLTENYCRNP 61
DB      275 TPVQDCYHGDGSRYSIGISSTVTGRTCCSSMIPHHORTPENYPNAGLTENYCRNP 334
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QY      62 SGKQPCYTTDPCVRWEYCNLTQCSSETS 90
DB      335 ADKGPWCFTTDPBVRWEYCNLKKCSGTEA 363
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      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-946-893-4
/ Sequence 4, Application US/09946893
/ Patent No. US20020072494A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yihai
/ TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
/ FILE REFERENCE: Mewburn
US-09-946-893-4
```

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/ CURRENT APPLICATION NUMBER: US/09/946,893
/ CURRENT FILING DATE: 2001-09-05
/ PRIOR APPLICATION NUMBER: US 60/230,893
/ PRIOR FILING DATE: 2000-09-05
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-946-893-4

Query Match      78.5%; Score 423; DB 9; Length 458;
Best Local Similarity 78.7%; Pred. No. 1.5e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY      2 SPVQDCYHGDGSRYSIGISSTVTGRTCCSSMIPHHORTPENYPNAGLTENYCRNP 61
DB      269 TPVQDCYHGDGSRYSIGISSTVTGRTCCSSMIPHHORTPENYPNAGLTENYCRNP 328
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62 SGKQPCYTTDPCVRWEYCNLTQCSSETS 90
DB      329 ADKGPWCFTTDPBVRWEYCNLKKCSGTEA 357
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RESULT 12
US-09-946-893-5
/ Sequence 5, Application US/09946893
/ Patent No. US20020072494A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yihai
/ TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
/ FILE REFERENCE: Mewburn
/ CURRENT APPLICATION NUMBER: US/09/946,893
/ CURRENT FILING DATE: 2001-09-05
/ PRIOR APPLICATION NUMBER: US 60/230,893
/ PRIOR FILING DATE: 2000-09-05
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 569
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
US-09-946-893-5

Query Match      78.5%; Score 423; DB 9; Length 569;
Best Local Similarity 78.7%; Pred. No. 1.9e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY      2 SPVQDCYHGDGSRYSIGISSTVTGRTCCSSMIPHHORTPENYPNAGLTENYCRNP 61
DB      371 TPVQDCYHGDGSRYSIGISSTVTGRTCCSSMIPHHORTPENYPNAGLTENYCRNP 430
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62 SGKQPCYTTDPCVRWEYCNLTQCSSETS 90
DB      431 ADKGPWCFTTDPBVRWEYCNLKKCSGTEA 459
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      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-946-893-8
/ Sequence 8, Application US/09946893
/ Patent No. US20020072494A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yihai
/ TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
/ FILE REFERENCE: Mewburn
/ CURRENT APPLICATION NUMBER: US/09/946,893
/ CURRENT FILING DATE: 2001-09-05
/ PRIOR APPLICATION NUMBER: US 60/230,893
US-09-946-893-8
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; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
; OTHER INFORMATION: with a tumor targeting signal peptide
US-09-946-893-8

Query Match 78.5%; Score 423; DB 9; Length 571;
Best Local Similarity 78.7%; Pred. No. 1.9e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDRGRYRGISSTVTGRTCSWSSMTPHMQRTPENYPNAGLTENTYCRNP 61
DB 371 TPVVDCHGDRGRYRGISSTVTGRTCSWSSMTPHMQRTPENYPNAGLTENTYCRNP 430

QY 62 SGKQPMCYTTDPCVRMEYCNLTQCSSETS 90
DB 431 ADKGPWCFTTDPVSVRMEYCNLTQCSSETS 459

RESULT 14
US-09-946-893-6

; Sequence 6, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Meuburn
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
; OTHER INFORMATION: with a tumor targeting signal
US-09-946-893-6

Query Match 78.5%; Score 423; DB 9; Length 576;
Best Local Similarity 78.7%; Pred. No. 1.9e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDRGRYRGISSTVTGRTCSWSSMTPHMQRTPENYPNAGLTENTYCRNP 61
DB 371 TPVVDCHGDRGRYRGISSTVTGRTCSWSSMTPHMQRTPENYPNAGLTENTYCRNP 430

QY 62 SGKQPMCYTTDPCVRMEYCNLTQCSSETS 90
DB 431 ADKGPWCFTTDPVSVRMEYCNLTQCSSETS 459

RESULT 15
US-09-967-386-1

; Sequence 1, Application US/09967386
; Patent No. US2002015992A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Henkin, Jack
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
; TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
; FILE REFERENCE: 6738 US.02

; CURRENT APPLICATION NUMBER: US/09/967,386
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/236,550
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-967-386-1

Query Match 78.5%; Score 423; DB 10; Length 791;
Best Local Similarity 78.7%; Pred. No. 2.6e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDRGRYRGISSTVTGRTCSWSSMTPHMQRTPENYPNAGLTENTYCRNP 61
DB 352 TPVVDCHGDRGRYRGISSTVTGRTCSWSSMTPHMQRTPENYPNAGLTENTYCRNP 411

QY 62 SGKQPMCYTTDPCVRMEYCNLTQCSSETS 90
DB 412 ADKGPWCFTTDPVSVRMEYCNLTQCSSETS 440

Search completed: January 12, 2004, 17:29:39
Job time : 27.6842 secs

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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:21:34 : Search time 13 Seconds
(without alignments)
296.176 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539
Sequence: 1 KSPVQDCHGDGRSYRGIS.....DPCVMEYCNLTQCESTSG 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
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6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	425	78.8	810 4	US-08-991-761A-11 Sequence 11, Appl
2	423	78.5	374 4	US-09-377-250-3 Sequence 3, Appl
3	423	78.5	375 4	US-09-377-250-2 Sequence 2, Appl
4	423	78.5	378 2	US-08-612-788-42 Sequence 42, Appl
5	423	78.5	378 3	US-09-066-028-42 Sequence 42, Appl
6	423	78.5	378 3	US-09-066-059-1 Sequence 1, Appl
7	423	78.5	378 4	US-09-335-325-42 Sequence 42, Appl
8	423	78.5	451 4	US-09-377-250-1 Sequence 1, Appl
9	423	78.5	452 4	US-09-377-250-1 Sequence 4, Appl
10	423	78.5	790 1	US-08-469-486-54 Sequence 54, Appl
11	423	78.5	790 2	US-08-469-658-54 Sequence 54, Appl
12	423	78.5	791 1	US-08-643-219-1 Sequence 1, Appl
13	423	78.5	791 2	US-09-131-995-1 Sequence 1, Appl
14	423	78.5	791 3	US-08-832-087B-1 Sequence 1, Appl
15	423	78.5	791 3	US-08-851-350-1 Sequence 1, Appl
16	423	78.5	791 3	US-09-132-154-1 Sequence 1, Appl
17	423	78.5	791 4	US-08-991-761A-6 Sequence 6, Appl
18	423	78.5	810 1	US-07-854-603-2 Sequence 2, Appl
19	423	78.5	810 3	US-08-147-000B-29 Sequence 29, Appl
20	423	78.5	810 3	US-09-086-514-1 Sequence 1, Appl
21	423	78.5	810 4	US-09-192-012-5 Sequence 5, Appl
22	423	78.5	810 6	5200340-8 Patent No. 5200340
23	423	78.5	814 1	US-08-750-711-1 Sequence 1, Appl
24	413	76.6	812 4	US-08-991-761A-7 Sequence 7, Appl
25	410	76.1	352 2	US-08-612-788-40 Sequence 40, Appl
26	410	76.1	352 3	US-09-066-028-40 Sequence 40, Appl
27	410	76.1	352 4	US-09-335-325-40 Sequence 40, Appl

28	405	75.1	84 4	US-09-348-953-2 Sequence 2, Appl
29	402	74.6	790 4	US-08-991-761A-13 Sequence 13, Appl
30	388	72.0	378 2	US-08-612-788-41 Sequence 41, Appl
31	388	72.0	378 3	US-09-066-028-41 Sequence 41, Appl
32	388	72.0	378 4	US-09-335-325-41 Sequence 41, Appl
33	388	72.0	398 4	US-09-192-012-2 Sequence 1, Appl
34	388	72.0	812 1	US-08-451-932-1 Sequence 1, Appl
35	388	72.0	812 1	US-08-451-932-1 Sequence 1, Appl
36	388	72.0	812 1	US-08-452-260-1 Sequence 1, Appl
37	388	72.0	812 1	US-08-326-785-1 Sequence 1, Appl
38	388	72.0	812 2	US-08-612-788-1 Sequence 1, Appl
39	388	72.0	812 2	US-08-605-598B-1 Sequence 1, Appl
40	388	72.0	812 2	US-08-429-743-1 Sequence 1, Appl
41	388	72.0	812 2	US-08-866-735-1 Sequence 1, Appl
42	388	72.0	812 3	US-09-066-028-1 Sequence 1, Appl
43	388	72.0	812 4	US-09-192-012-3 Sequence 3, Appl
44	388	72.0	812 4	US-09-335-325-1 Sequence 1, Appl
45	388	72.0	812 4	US-08-991-761A-12 Sequence 12, Appl

ALIGNMENTS

```
RESULT 1
US-08-991-761A-11
; Sequence 11, Application US/08991761A
; Patent No. 6576609
;
; GENERAL INFORMATION:
; APPLICANT: Soft, Gerald
; APPLICANT: Gately, Stephen
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: "Methods and Compositions for Generating
; TITLE OF INVENTION: Angiotatin"
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,761A
; FILING DATE:
; CLASSIFICATION: 1642
; ATTORNEY/AGENT INFORMATION:
; NAME: Crook, Wanneil M.
; REGISTRATION NUMBER: 31,071
; REFERENCE/DOCKET NUMBER: 3501-16-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 810 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-991-761A-11
;
; Query Match 78.8%; Score 425; DB 4; Length 810;
; Best Local Similarity 77.3%; Pred. No. 1.3e-37;
; Matches 68; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
;
; QY 2 SPVVQDCHGDGRSYRGISITVTGRTQSWSSMTPIHWQRTPEVYPAAGLTENYCRNPD 61
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; Db 371 TPVQDCHGDGRSYRGISITVTGRTQSWSSMTPIHWQRTPEVYPAAGLTENYCRNPD 430
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QY 62 SGKQPCWCTTDPVCRWEYCNLTQCSETE 89
DB 431 ADKGPWCFTTDPVCRWEYCNLTQCSGTE 458

RESULT 2

US-09-377-250-3
Sequence 3, Application US/09377250
Patent No. 6365364
GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
APPLICANT: SMORDS JENNY, NANCY
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
FILE REFERENCE: 48409/360
CURRENT APPLICATION NUMBER: US/09/377,250
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: angiogenesis inhibitor
NAME/KEY: MOD RES
LOCATION: (264)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-3

Query Match 78.5%; Score 423; DB 4; Length 374;
Best Local Similarity 78.7%; Pred. No. 8.8e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 61
DB 274 TPVVDCCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 333

QY 62 SGKQPCWCTTDPVCRWEYCNLTQCSETE 90
DB 334 ADKGPWCFTTDPVCRWEYCNLTQCSGTEA 362

RESULT 3

US-09-377-250-2
Sequence 2, Application US/09377250
Patent No. 6365364
GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
APPLICANT: SMORDS JENNY, NANCY
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
FILE REFERENCE: 48409/360
CURRENT APPLICATION NUMBER: US/09/377,250
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: angiogenesis inhibitor
NAME/KEY: MOD RES
LOCATION: (265)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-2

Query Match 78.5%; Score 423; DB 4; Length 375;
Best Local Similarity 78.7%; Pred. No. 8.8e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 61
DB 275 TPVVDCCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 334

QY 62 SGKQPCWCTTDPVCRWEYCNLTQCSETE 90
DB 335 ADKGPWCFTTDPVCRWEYCNLTQCSGTEA 363

RESULT 4

US-08-612-788-42
Sequence 42, Application US/08612788
Patent No. 5837682
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Jones & Askew
STREET: 191 Peachtree Street, 37th floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: KL-4BKLS
US-08-612-788-42

Query Match 78.5%; Score 423; DB 2; Length 378;
Best Local Similarity 78.7%; Pred. No. 8.9e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 61
DB 279 TPVVDCCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 338

QY 62 SGKQPCWCTTDPVCRWEYCNLTQCSETE 90
DB 339 ADKGPWCFTTDPVCRWEYCNLTQCSGTEA 367

RESULT 5

US-09-066-028-42
; Sequence 42, Application US/0906028
; Patent No. 6024688
; GENERAL INFORMATION:
; APPLICANT: Folkmann, M. Judah
; APPLICANT: O'Reilly, Micheal
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, B. Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,028
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; REFERENCE/DOCKET NUMBER: 05213-0126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: K1-4BKLS
; US-09-066-028-42

Query Match 78.5%; Score 423; DB 3; Length 378;
Best Local Similarity 78.7%; Pred. No. 8.9e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDSYRGISSTTTGRTGQSSMTPHHORTPENYPNAGLTENYCRNPD 61
DB 279 TPVVDCHGDSYRGISSTTTGRTGQSSMTPHHORTPENYPNAGLTENYCRNPD 338
QY 62 SGKOPWCYTTDPCVWWEYCNLTQCSSETS 90
DB 339 ADKGPWCFTTDPVWWEYCNLTQCSSETS 367

RESULT 6
US-09-206-059-1
; Sequence 1, Application US/09206059
; Patent No. 6201104
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Nicholas
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiogenesis-inhibiting Protein Binding Peptides and

; TITLE OF INVENTION: Proteins and Methods of Use
; FILE REFERENCE: 05213-0370
; CURRENT APPLICATION NUMBER: US/09/206,059
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-206-059-1

Query Match 78.5%; Score 423; DB 3; Length 378;
Best Local Similarity 78.7%; Pred. No. 8.9e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDSYRGISSTTTGRTGQSSMTPHHORTPENYPNAGLTENYCRNPD 61
DB 279 TPVVDCHGDSYRGISSTTTGRTGQSSMTPHHORTPENYPNAGLTENYCRNPD 338
QY 62 SGKOPWCYTTDPCVWWEYCNLTQCSSETS 90
DB 339 ADKGPWCFTTDPVWWEYCNLTQCSSETS 367

RESULT 7
US-09-335-325-42
; Sequence 42, Application US/09335325
; Patent No. 6521439
; GENERAL INFORMATION:
; APPLICANT: Folkmann, M. Judah
; APPLICANT: O'Reilly, Micheal
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, B. Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/335,325
; FILING DATE: 17-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,788
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; REFERENCE/DOCKET NUMBER: 05213-0126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K1-48LKS
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-335-325-42

Query Match 78.5%; Score 423; DB 4; Length 378;
Best Local Similarity 78.7%; Pred. No. 8,9e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDGCHGDDGSRYSIGSTTTGRTCCQSSMTPHMQRTPEPNAGLTENYCRNP 61
DB 279 TPVVDGCHGDDGSRYSIGSTTTGRTCCQSSMTPHMQRTPEPNAGLTENYCRNP 338

QY 62 SGKOPWCYTTPDCVRMEYCNLTQCSSETS 90
DB 339 ADKGPWCFTTDPVSRMEYCNLKKCSGTEA 367

RESULT 8

US-09-377-250-1

Sequence 1, Application US/09377250
Patent No. 6365364

GENERAL INFORMATION:

APPLICANT: MANN, KENNETH G.

APPLICANT: SMORDS JENNY, NANCY

TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF

FILE REFERENCE: 48409/360

CURRENT APPLICATION NUMBER: US/09/377,250

CURRENT FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 451

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: plasminogen fragment

NAME/KEY: MOD RES

LOCATION: (53)

OTHER INFORMATION: Xaa = Gln or Glu

NAME/KEY: MOD RES

LOCATION: (341)

OTHER INFORMATION: Xaa = Gln or Glu

US-09-377-250-1

Query Match 78.5%; Score 423; DB 4; Length 451;
Best Local Similarity 78.7%; Pred. No. 1,1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDGCHGDDGSRYSIGSTTTGRTCCQSSMTPHMQRTPEPNAGLTENYCRNP 61
DB 351 TPVVDGCHGDDGSRYSIGSTTTGRTCCQSSMTPHMQRTPEPNAGLTENYCRNP 410

QY 62 SGKOPWCYTTPDCVRMEYCNLTQCSSETS 90
DB 411 ADKGPWCFTTDPVSRMEYCNLKKCSGTEA 439

RESULT 9

US-09-377-250-4

Sequence 4, Application US/09377250
Patent No. 6365364

GENERAL INFORMATION:

APPLICANT: MANN, KENNETH G.

APPLICANT: SMORDS JENNY, NANCY

TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF

FILE REFERENCE: 48409/360

CURRENT APPLICATION NUMBER: US/09/377,250

CURRENT FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 4

LENGTH: 452

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: plasminogen fragment

NAME/KEY: MOD RES

LOCATION: (53)

OTHER INFORMATION: Xaa = Gln or Glu

FEATURE:

NAME/KEY: MOD RES

LOCATION: (342)

OTHER INFORMATION: Xaa = Gln or Glu

Query Match 78.5%; Score 423; DB 4; Length 452;
Best Local Similarity 78.7%; Pred. No. 1,1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDGCHGDDGSRYSIGSTTTGRTCCQSSMTPHMQRTPEPNAGLTENYCRNP 61
DB 352 TPVVDGCHGDDGSRYSIGSTTTGRTCCQSSMTPHMQRTPEPNAGLTENYCRNP 411

QY 62 SGKOPWCYTTPDCVRMEYCNLTQCSSETS 90
DB 412 ADKGPWCFTTDPVSRMEYCNLKKCSGTEA 440

RESULT 10

US-08-469-486-54

Sequence 54, Application US/08469486
Patent No. 5739281

GENERAL INFORMATION:

APPLICANT: Thoegeisen, Hans Christian

APPLICANT: Hollet, Thor Laas

APPLICANT: Etzerodt, Michael

TITLE OF INVENTION: Improved method for the refolding of

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,486

FILING DATE:

CLASSIFICATION: 530

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/192,060

FILING DATE: February 4, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 06363/002001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617 542 5070

TELEFAX: 617 542 8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:

LENGTH: 790 amino acids

TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-54

Query Match 78.5%; Score 423; DB 1; Length 790;
Best Local Similarity 78.7%; Pred. No. 2.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHOKTPENYPNAGLTMYNCRNP 61
DB 351 TPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHOKTPENYPNAGLTMYNCRNP 410
QY 62 SGKOPMCYTTDPCVMEYCNLTQCSSETS 90
DB 411 ADKGPWCFTTDPVSVMWEYCNLKKCSGTEA 439

RESULT 11

US-08-469-658-54
Sequence 54, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Th egersten, Hans Christian
APPLICANT: Holteit, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-658-54

Query Match 78.5%; Score 423; DB 2; Length 790;
Best Local Similarity 78.7%; Pred. No. 2.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 2 SPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHOKTPENYPNAGLTMYNCRNP 61
DB 351 TPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHOKTPENYPNAGLTMYNCRNP 410

DB 351 TPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHOKTPENYPNAGLTMYNCRNP 410
QY 62 SGKOPMCYTTDPCVMEYCNLTQCSSETS 90
DB 411 ADKGPWCFTTDPVSVMWEYCNLKKCSGTEA 439

RESULT 12

US-08-643-219-1
Sequence 1, Application US/08643219
Patent No. 5801146
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,219
FILING DATE: 06-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Casullo, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
US-08-643-219-1

Query Match 78.5%; Score 423; DB 1; Length 791;
Best Local Similarity 78.7%; Pred. No. 2.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHOKTPENYPNAGLTMYNCRNP 61
DB 352 TPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHOKTPENYPNAGLTMYNCRNP 411
QY 62 SGKOPMCYTTDPCVMEYCNLTQCSSETS 90
DB 412 ADKGPWCFTTDPVSVMWEYCNLKKCSGTEA 440

RESULT 13

US-09-131-995-1
Sequence 1, Application US/09131995
Patent No. 5972896
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
US-09-131-995-1

Query Match 78.5%; Score 423; DB 2; Length 791;
Best Local Similarity 78.7%; Pred. No. 2,1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVODCYHGDGRSYRGISSTVTGRTCSQSSSMIPHHORTPENYNNAGLTENYCRND 61
DB 352 TPVODCYHGDGRSYRGISSTVTGRTCSQSSSMIPHHOKTPENYNNAGLTENYCRND 411

QY 62 SGKOPWCYTTDPCVRWEYCNLTQCSSETS 90
DB 412 ADKGPWCFTTDPSPVRWEYCNLKKCSGTEA 440

RESULT 14
US-08-832-087B-1
Sequence 1, Application US/08832087B
Patent No. 5981484
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
NUMBER OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087B
FILING DATE: 03-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
US-08-832-087B-1

Query Match 78.5%; Score 423; DB 2; Length 791;
Best Local Similarity 78.7%; Pred. No. 2,1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVODCYHGDGRSYRGISSTVTGRTCSQSSSMIPHHORTPENYNNAGLTENYCRND 61
DB 352 TPVODCYHGDGRSYRGISSTVTGRTCSQSSSMIPHHOKTPENYNNAGLTENYCRND 411

QY 62 SGKOPWCYTTDPCVRWEYCNLTQCSSETS 90
DB 412 ADKGPWCFTTDPSPVRWEYCNLKKCSGTEA 440

RESULT 15
US-08-851-350-1
Sequence 1, Application US/08851350
Patent No. 6057122
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
POLYNUCLEOTIDES ENCODING SAME AND METHODS
FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,350
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623

TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 791 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; US-08-851-350-1

Query Match 78.5%; Score 423; DB 3; Length 791;
Best Local Similarity 78.7%; Pred. No. 2.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVODCYHGDGRSYRGISSTVTGRTCSWSSMTPHMHQRTPENYPNAGLTENYCRNPD 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 352 TPVODCYHGDGQSYRGISSTVTGRTCSWSSMTPHRHQRTPENYPNAGLTENYCRNPD 411
QY 62 SGKQPCYTTDPCVMEYCNLTQCSSTES 90
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 412 ADKGPWCFTTDPVMEYCNLTQCSSTEA 440

Search completed: January 12, 2004, 17:27:15
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:19:12 ; Search time 12.0451 Seconds
(Without alignments)
710.580 Million cell updates/sec

Title: US-10-088-548-6

Sequence: 1 VRQCYHGNGQSYRGFTFTV.....SIRWEXCNLTRCSDEGTGV 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616882 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	98.9	4548	1 S00657	apoprotein(a) (EC
2	476	91.4	1420	1 A32869	apolipoprotein(a)
3	444	84.9	810	1 PLHU	plasma (EC 3.4.21
4	433	82.8	810	2 B30848	plasma (EC 3.4.21
5	415	79.3	812	1 PLBO	plasma (EC 3.4.21
6	413	79.0	120	2 E61545	plasma (EC 3.4.21
7	407	77.8	123	2 C61545	plasma (EC 3.4.21
8	401	76.7	790	1 PLRG	plasma (EC 3.4.21
9	400	76.5	812	1 PLMS	plasma (EC 3.4.21
10	392	75.0	810	2 B15260	plasma (EC 3.4.21
11	388	74.2	460	2 B61545	plasma (EC 3.4.21
12	381.5	72.9	169	2 A40522	plasma (EC 3.4.21
13	380	72.7	455	2 A61545	plasma (EC 3.4.21
14	354	67.7	89	2 A60140	plasma (EC 3.4.21
15	303	57.9	2869	2 T18518	apolipoprotein(a)
16	272.5	52.1	716	1 A40332	macrophage-stimula
17	269	51.4	728	1 JH0579	macrophage-stimula
18	268.5	51.3	716	1 JCS061	macrophage-stimula
19	263	50.3	728	1 A35644	macrophage-stimula
20	263	50.3	728	1 A60185	hepatocyte growth
21	247.5	47.3	711	1 A47136	hepatocyte growth
22	246.5	47.1	710	1 I51283	hepatocyte growth
23	242	46.3	411	2 I51285	hepatocyte growth
24	237.5	45.4	946	1 A47299	ret-related recept
25	216.5	41.4	943	2 B45082	neurotrophic recep
26	205	39.2	336	2 S33879	plasma precursor
27	204.5	39.1	622	1 TBHU	chromin (EC 3.4.2
28	204	39.0	625	1 TBBO	chromin (EC 3.4.2
29	201.5	38.5	617	2 S10511	chromin (EC 3.4.2

30	199.5	38.1	618	2 A35827	chromin (EC 3.4.2
31	193.5	37.0	603	2 S28941	coagulation factor
32	191.5	36.6	937	2 A45082	neurotrophic recep
33	189.5	36.2	560	1 UC4795	plasma hyaluronan
34	189	36.1	562	1 UKHUT	coagulation factor
35	188.5	36.0	615	1 KFHU12	plasma hyaluronan
36	174.5	33.4	558	2 JC5878	coagulation factor
37	173	33.1	559	1 A35029	t-plasminogen acti
38	173	33.1	559	1 A29941	t-plasminogen acti
39	171.5	32.8	432	1 S18932	u-plasminogen acti
40	170	32.5	655	1 A46888	hepatocyte growth
41	166.5	31.8	593	2 S45281	coagulation factor
42	160	30.6	433	1 UKBAY	u-plasminogen acti
43	159	30.4	431	2 JS0599	t-plasminogen acti
44	159	30.4	477	1 A34369	t-plasminogen acti
45	159	30.4	477	2 JS0598	t-plasminogen acti

ALIGNMENTS

RESULT 1
S00657
apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #ext change 08-Dec-2000
C:Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65266
R:McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Scam
Nature 330, 132-137, 1987
A>Title: CDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A:Reference number: S00657; MUID:88039109; PMID:3670400
A:Accession: S00657
A:Molecule type: mRNA
A:Residues: 1-4548 <MCL>
A:Cross-references: GB:X06290; EMBL:X06696; NID:928619; PIDN:CAA29618.1; PID:928620
R:Eaton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A>Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A:Reference number: A28017; MUID:87204109; PMID:3472206
A:Accession: A28017
A:Molecule type: Protein
A:Residues: 20-21,'P',23-34;177-179,'N',181-186,'T',188-196,'DKG',200;292-314,'W',316-3
X',4396-4401 <EXT>
R:Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meier, K.; Schwartz,
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A>Title: 5' control regions of the apolipoprotein(a) gene and members of the related p
A:Reference number: A47277; MUID:93165698; PMID:7679504
A:Accession: A47277
A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:L07899; NID:9967973; PID:9967974
R:Magaraci, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Se
Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A>Title: Characterization by yeast artificial chromosome cloning of the linked apolip
A:Reference number: A47233; MUID:93087573; PMID:1454851
A:Accession: A47233
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M60078; NID:9178786; PIDN:AAA5547.1; PID:9553188
A>Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: A47233
A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M60079; NID:9178784; PIDN:AAA5546.1; PID:9553187
R:Richiome, A
Biochemistry 31, 3113-3118, 1992
A>Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associ
A:Reference number: I52415; MUID:92207924; PMID:1554698
A:Accession: I52415

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RB4>
 A:Cross-references: GB:M86877; NID:g178780; PIDN:AA84909.1; PID:g553185
 A:Note: apo(a) gene 1 (nomenclature of reference I52415)
 A:Accession: I52415
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RB4>
 A:Cross-references: GB:M86878; NID:g178782; PIDN:AA51749.1; PID:g553186
 C:Genetics:
 A:Gene: GDB:IPA
 A:Cross-references: GDB:120699; OMIM:152200
 A:Map position: 6q26-6q27
 A:Note: several genes closely linked on chromosome 6 are identical in the first coding
 A:Note: repeats
 C:Superfamily: apolipoprotein(a); kringe homology; trypsin homology
 C:Keywords: hydrolase; kringe; lipid binding; lipoprotein; serine proteinase
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-4548/Product: apolipoprotein(a) #status experimental <MAT>
 F:28-105/Domain: kringe homology <KR1>
 F:142-219/Domain: kringe homology <KR2>
 F:256-333/Domain: kringe homology <KR3>
 F:370-447/Domain: kringe homology <KR4>
 F:484-561/Domain: kringe homology <KR5>
 F:598-675/Domain: kringe homology <KR6>
 F:712-789/Domain: kringe homology <KR7>
 F:826-903/Domain: kringe homology <KR8>
 F:940-1017/Domain: kringe homology <KR9>
 F:1054-1131/Domain: kringe homology <KR10>
 F:1168-1245/Domain: kringe homology <KR11>
 F:1282-1359/Domain: kringe homology <KR12>
 F:1396-1473/Domain: kringe homology <KR13>
 F:1510-1587/Domain: kringe homology <KR14>
 F:1624-1701/Domain: kringe homology <KR15>
 F:1738-1815/Domain: kringe homology <KR16>
 F:1852-1929/Domain: kringe homology <KR17>
 F:1966-2043/Domain: kringe homology <KR18>
 F:2080-2157/Domain: kringe homology <KR19>
 F:2194-2271/Domain: kringe homology <KR20>
 F:2308-2385/Domain: kringe homology <KR21>
 F:2422-2499/Domain: kringe homology <KR22>
 F:2536-2613/Domain: kringe homology <KR23>
 F:2650-2727/Domain: kringe homology <KR24>
 F:2764-2841/Domain: kringe homology <KR25>
 F:2878-2955/Domain: kringe homology <KR26>
 F:2992-3069/Domain: kringe homology <KR27>
 F:3106-3183/Domain: kringe homology <KR28>
 F:3320-3297/Domain: kringe homology <KR29>
 F:3334-3411/Domain: kringe homology <KR30>
 F:3448-3525/Domain: kringe homology <KR31>
 F:3562-3639/Domain: kringe homology <KR32>
 F:3676-3753/Domain: kringe homology <KR33>
 F:3782-3859/Domain: kringe homology <KR34>
 F:3896-3973/Domain: kringe homology <KR35>
 F:4010-4087/Domain: kringe homology <KR36>
 F:4124-4201/Domain: kringe homology <KR37>
 F:4228-4307/Domain: kringe homology <KR38>
 F:4328-4541/Domain: trypsin homology <TRY>

Query Match 98.9%; Score 517; DB 1; Length 4548;
 Best Local Similarity 98.9%; Pred. No. 2,2e+44;
 Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRQCYHNGSGSYRGFTSTVTGRTCSWSMTPHRHQRTPEPNYNDGLTMNYCNPADT 60
 DB 4121 VRQCYHNGSGSYRGFTSTVTGRTCSWSMTPHRHQRTPEPNYNDGLTMNYCNPADT 4180

QY 61 GPCFTTDPDSIRWEYCNLTRCSDEGTIV 89
 DB 4181 GPCFTTDPDSIRWEYCNLTRCSDEGTIV 4209

RESULT 2
 A32869
 apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text_change 22-Jun-1999
 C:Accession: A32869; A30848
 J:Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
 J: Biol. Chem. 264, 5957-5965, 1989
 A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis
 A:Reference number: A32869; MUID:89174660; PMID:2925643
 A:Accession: A32869
 A:Molecule type: mRNA
 A:Residues: 1-1420 <TOM>
 A:Cross-references: GB:J04635; NID:g342072; PIDN:AA36833.1; PID:g342073
 C:Superfamily: apolipoprotein(a); kringe homology; trypsin homology
 C:Keywords: hydrolase; kringe; lipid binding; lipoprotein; serine proteinase
 F:50-127/Domain: kringe homology <KR1>
 F:164-241/Domain: kringe homology <KR2>
 F:278-355/Domain: kringe homology <KR3>
 F:392-469/Domain: kringe homology <KR4>
 F:506-583/Domain: kringe homology <KR5>
 F:620-697/Domain: kringe homology <KR6>
 F:726-803/Domain: kringe homology <KR7>
 F:840-917/Domain: kringe homology <KR8>
 F:954-1031/Domain: kringe homology <KR9>
 F:1068-1145/Domain: kringe homology <KR10>
 F:1191-1413/Domain: trypsin homology <TRY>

Query Match 91.4%; Score 478; DB 2; Length 1420;
 Best Local Similarity 91.0%; Pred. No. 6,7e+41;
 Matches 81; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 VRQCYHNGSGSYRGFTSTVTGRTCSWSMTPHRHQRTPEPNYNDGLTMNYCNPADT 60
 DB 1065 VRQCYHNGSGSYRGFTSTVTGRTCSWSMTPHRHQRTPEPNYNDGLTMNYCNPADT 1124

QY 61 GPCFTTDPDSIRWEYCNLTRCSDEGTIV 89
 DB 1125 GPCFTTDPDSIRWEYCNLTRCSDEGTIV 1153

RESULT 3
 PLNU
 plasmin (EC 3.4.21.7) precursor [validated] - human
 N:Alternate names: plasminogen precursor [misnomer]
 N:Contents: angiotensin; microplasmin; plasminogen
 C:Species: Homo sapiens (man)
 C:Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text_change 15-Sep-2000
 C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A046
 J:Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
 J: Biol. Chem. 265, 6104-6111, 1990
 A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibrin
 A:Reference number: A35229; MUID:90202879; PMID:2318848
 A:Accession: A35229
 A:Molecule type: DNA
 A:Residues: 1-810 <PET>
 A:Cross-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; PID:g387026
 A:Experimental source: leukocyte; lung fibroblast
 R:Malgaroli, N.; Bruno, L.; Pontoglio, M.; Cardini, G.; Meroni, G.; Ottolenghi, S.; Tai
 Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
 A:Title: Definition of the transcription initiation site of human plasminogen gene in 11v
 A:Reference number: I52242; MUID:91097523; PMID:2268308
 A:Accession: I52242
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <MAL>
 A:Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613
 R:Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
 FEBS Lett. 213, 254-260, 1987
 A:Title: Molecular cloning and characterization of a full-length cDNA clone for human pl
 A:Reference number: A26646; MUID:87162490; PMID:3030813
 A:Accession: A26646
 A:Molecule type: mRNA

A:Residues: 1-471, 'D', 473-810 <FOR>
A:Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
A:Experimental source: liver
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A:Reference number: 145961; WUID:85023311; PMID:6148961
A:Accession: 162738
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471, 'D', 473-810 <MAL2>
A:Cross-references: GB:X02922; NID:g190112; PIDN:AAA60124.1; PID:g387031
A:Accession: 184609
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL3>
A:Cross-references: GB:X02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
R:Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
A:Reference number: S03735; WUID:81212097; PMID:7238497
A:Accession: S03735
A:Molecule type: protein
A:Residues: 20-71, 'E', 73-76 <BRU>
R:Sortrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A:Reference number: A00929
A:Accession: A00929
A:Molecule type: protein
A:Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>
R:Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A:Title: Primary structure of the B-chain of human plasmin.
A:Reference number: A04627; WUID:77225245; PMID:142009
A:Accession: A04627
A:Molecule type: protein
A:Residues: 581-810 <WII>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human pl
A:Reference number: A04625; WUID:75093329; PMID:122932
A:Accession: A04625
A:Molecule type: protein
A:Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <WII>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha
A:Reference number: A04626; WUID:76043692; PMID:126863
A:Accession: A04626
A:Molecule type: protein
A:Residues: 483-507, 'E', 509-604 <WII>
R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A:Title: The primary structure of human plasminogen. II. The histidine loop of human pla
A:Reference number: A92125; WUID:73149248; PMID:4694729
A:Contents: annotation: active site
R:Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A:Reference number: A92048; WUID:69234739; PMID:4420117
A:Contents: annotation: active site
R:Trexler, M.; Vali, Z.; Patchy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A:Reference number: A93382; WUID:6213905; PMID:6919539
A:Contents: annotation: omega-aminocarboxylic acid binding sites
R:Vali, Z.; Patchy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A:Reference number: A92458; WUID:85054794; PMID:6094526
A:Contents: annotation: fibrin binding site; omega-aminocarboxylic acid binding site
R:Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marit, D.; Soehndel, S.; McCance, S.G.;

J. Biol. Chem. 271, 29461-29467, 1996
A:Title: Kringle domains of human angiotensin. Characterization of the anti-proliferative
A:Reference number: A58811; WUID:97067211; PMID:8910613
A:Contents: annotation
R:Uhlen, H.R.; Uggv, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A:Title: Generation of an angiotensin-like fragment from plasminogen by streptolysin-1 (M
A:Reference number: A58812; WUID:9548733; PMID:9548733
A:Contents: annotation
R:Tulinsky, A.; Mulichak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51341; PDB:1PK4
A:Contents: annotation: X-ray crystallography, 1.9 angstroms, residues 376-454
R:Tulinsky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51488; PDB:2PK4
A:Contents: annotation: X-ray crystallography, 2.25 angstroms, residues 375-454
R:Wu, T.P.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A:Reference number: A51911; PDB:1PKR
A:Contents: annotation: X-ray crystallography, 2.48 angstroms, residues 102-181
R:Padmanabhan, K.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A:Reference number: A52408; PDB:1PMK
A:Contents: annotation: X-ray crystallography, 2.25 angstroms, residues 377-454
R:Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65244; PDB:1CEA
A:Contents: annotation: X-ray crystallography, 2.1 angstroms, residues 102-181
R:Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65245; PDB:1CEB
A:Contents: annotation: X-ray crystallography, 2.1 angstroms, residues 102-181
R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 A
A:Reference number: A58819; WUID:92031502; PMID:1657148
A:Contents: annotation
R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
A:Reference number: A58818; WUID:92031503; PMID:1657149
A:Contents: annotation
R:de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.I.
Biochemistry 31, 270-279, 1992
A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4
A:Reference number: A39483; WUID:92118803; PMID:1310033
A:Contents: annotation: X-ray crystallography, 2.4 angstroms
R:Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A:Reference number: A65980; PDB:1KRN
A:Contents: annotation: X-ray crystallography, 1.67 angstroms, residues 376-454
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65803; PDB:1HPJ
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A:Reference number: A43645; WUID:94237157; PMID:8181475
A:Contents: annotation: conformation by (1)H-NMR, residues 96-184
R:Rejzante, M.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminoge
A:Reference number: A58817; WUID:94237158; PMID:8181476
A:Contents: annotation: conformation by (1)H-NMR
C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many oth
d PIR:FGHGB).

C/Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately after 580, resulting in two chains connected by two disulfide bonds. Without the inhibitor, C/Comment: Microplasmin is formed by autocatalytic cleavage of plasmin under artificial conditions. C/Comment: Stremoplasmin (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. C/Comment: C/Genetics: A:Gene: GDB:PLG A:Cross-references: GDB:119498; OMIM:173350 A:Map position: 6q25-6q27 A:Functions: 11/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529 C/Function: A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the graafian follicle; also activates the urokinase-type plasminogen activator; fibrinolysis A:Pathway: fibrinolysis C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology C/Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolysis; plasminogen-related protein precursor homology <PLPH> F/1-96/Domain: signal sequence #status predicted <SIG> F/1-19/Domain: signal sequence #status predicted <SIG> F/20-810/Product: plasminogen #status experimental <PRO> F/20-96/Domain: activation peptide #status experimental <APT> F/29-466/Product: angiotensin #status experimental <AST> F/77-580/Product: plasmin #status experimental <MAT> F/97-580/Domain: plasmin chain A #status experimental <CHA> F/103-181/Domain: kringle homology <KR1> F/185-262/Domain: kringle homology <KR2> F/375-352/Domain: kringle homology <KR3> F/377-454/Domain: kringle homology <KR4> F/481-560/Domain: kringle homology <KR5> F/550-580,581-810/Product: microplasmin #status experimental <MMT>

Query Match Best Local Similarity 82.9%; Score 444; DB 1; Length 810; Pred. No. 1,2e-37; Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VRQCHNGNSYRGSTSTVTGRTCOSWSMTPHRHQRTPENYNDGLTMNCRNPDAQT 60
Db 374 VQCHNGDQSYRGSTSTVTGRTGKCSWSMTPHRHQRTPENYNDGLTMNCRNPDAQT 433
Qy 61 GPWCFTTDPISIRWEYCNLTRCSDETEGVV 89
Db 434 GPWCFTTDPISIRWEYCNLTRCSDETEGVV 462

RESULT 4

B30848 plasmin (EC 3.4.21.7) precursor - rhesus macaque
C/Species: Macaca mulatta (rhesus macaque)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C/Accession: B32869; B30848
R/Tomlinson, J.E.; McLean, J.W.; Lawm, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A>Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A/Reference number: A32869; MUID:89174660; PMID:2925643
A/Accession: B32869
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1810 <RNU>
A:Cross-references: GB:004697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C/Keywords: fibrinolysis; glycoprotein; hydrolysis; kringle; serine proteinase
F/1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F/1-9/Domain: signal sequence #status predicted <SIG>
F/103-181/Domain: kringle homology <KR1>
F/185-262/Domain: kringle homology <KR2>
F/375-352/Domain: kringle homology <KR3>
F/377-454/Domain: kringle homology <KR4>
F/481-560/Domain: kringle homology <KR5>
F/581-803/Domain: trypsin homology <TRY>
F/49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,332-352,665,760/Active site: His, Asp, Ser #status predicted
F/522,665,760/Active site: His, Asp, Ser #status predicted

Query Match 82.8%; Score 433; DB 2; Length 810;

Best Local Similarity 79.5%; Pred. No. 1,5e-36; Matches 70; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 VRQCHNGNSYRGSTSTVTGRTCOSWSMTPHRHQRTPENYNDGLTMNCRNPDAQT 60
Db 374 VQCHNGDQSYRGSTSTVTGRTGKCSWSMTPHRHQRTPENYNDGLTMNCRNPDAQT 433
Qy 61 GPWCFTTDPISIRWEYCNLTRCSDETEGVV 88
Db 434 GPWCFTTDPISIRWEYCNLTRCSDETEGVV 461

RESULT 5

PLBO plasmin (EC 3.4.21.7) precursor - bovine
N/Alternate names: plasminogen
C/Species: Bos primigenius taurus (cattle)
C/Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 18-Jun-1999
C/Accession: S45046; A25835; I45961; S03736
R/Berglund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A:Description: Cloning and characterization of the bovine plasminogen cDNA.
A/Reference number: S45046
A:Accession: S45046
A:Molecule type: mRNA
A:Residues: 1-812

A:Cross-references: EMBL:X79402; NID:g494962; PIDN:CAAS593.1; PID:g494963
A/Experimental source: liver
A/Note: It is uncertain whether Met-1 or Met-8 is the initiator
R/Schaller, J.; Moser, P.W.; Danneberg-Muller, G.A.K.; Rosselet, S.J.; Kamfer, U.; Rick
Eur. J. Biochem. 149, 267-278, 1985
A>Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmin
A/Reference number: A25835; MUID:85203906; PMID:3846532
A:Accession: A25835
A:Molecule type: protein
A:Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
R/Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A>Title: Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.
A/Reference number: I45961; MUID:85023311; PMID:6148961
A:Accession: I45961
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 706-743, 'R', 745-812 <MAL>
A:Cross-references: GB:K02935; NID:G163551; PIDN:AAA30714.1; PID:G163552
R/Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickl, E.B.; Lergler, W.; Manneberg, M.; Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, bovine, and rat plasminogen.
A/Reference number: S03735; MUID:81212097; PMID:7238497
A:Accession: S03736
A:Molecule type: protein
A:Residues: 27-83

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the graafian follicle; also activates the urokinase-type plasminogen activator; fibrinolysis A:Pathway: fibrinolysis C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology C/Keywords: duplication; fibrinolysis; glycoprotein; hydrolysis; kidney; kringle; plasma; F/1-26/Domain: signal sequence #status predicted <SIG> F/1-103/Domain: plasminogen-related protein precursor homology <PRO> F/27-103/Domain: activation peptide #status experimental <APT> F/104-583,584-812/Product: plasmin #status experimental <MAT> F/104-583/Domain: plasmin chain A #status experimental <ACH> F/110-188/Domain: kringle homology <KR1> F/192-269/Domain: kringle homology <KR2> F/282-359/Domain: kringle homology <KR3> F/384-461/Domain: kringle homology <KR4> F/485-564/Domain: kringle homology <KR5> F/584-812/Domain: trypsin homology <TRY> F/584-805/Domain: trypsin homology <TRY> F/56-80,60-68,110-188,131-171,159-185,192-269,195-323,213-252,241-264,282-359,303-342,332-352,665,760/Active site: His, Asp, Ser #status predicted

F:315/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:365/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 79.3%; Score 415; DB 1; Length 812;
Best Local Similarity 79.5%; Pred. No. 1,1e-34;
Matches 66; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 ROCYHNGOSYRGFTSTVTGRTCSQSWSMTPRHQRTPENYNDGLTMNYCRNPADTG 61
DB 382 QDCYHNGOSYRGFTSTVTGRTCSQSWSMTPRHQRTPENYNDGLTMNYCRNPADTG 441
QY 62 PWCFTTDPISIRWEYCNLTRCSDT 84
DB 442 PWCYTTDPISIRWEYCNLTRCSDT 464

RESULT 6

plasma (EC 3.4.21.7) precursor - dog (fragments)
N:Alternate names: plasminogen
C:Species: Canis lupus familiaris (dog)
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
C/Accession: B61545
R/Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A>Title: Structural aspects of the plasminogen of various species.
A/Reference number: A61545; MUID:8905015; PMID:3168975
A/Accession: B61545
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-120 <SCH>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C/Keywords: hydrolase; serine proteinase
F:37-114/Domain: kringle homology <KR4>

Query Match 79.0%; Score 413; DB 2; Length 120;
Best Local Similarity 74.7%; Pred. No. 2.6e-35;
Matches 65; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VROCYHNGOSYRGFTSTVTGRTCSQSWSMTPRHQRTPENYNDGLTMNYCRNPADTG 60
DB 34 VORCYHNGOSYRGFTSTVTGRTCSQSWSMTPRHQRTPENYNDGLTMNYCRNPADTG 93
QY 61 GPCFTTDPISIRWEYCNLTRCSDT 87
DB 94 SPWCYTTDPISIRWEYCNLTRCSDT 120

RESULT 7

plasma (EC 3.4.21.7) precursor - goat (fragments)
N:Alternate names: plasminogen
C:Species: Capra aegagrus hircus (domestic goat)
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
C/Accession: C61545
R/Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A>Title: Structural aspects of the plasminogen of various species.
A/Reference number: A61545; MUID:8905015; PMID:3168975
A/Accession: C61545
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-123 <SCH>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C/Keywords: hydrolase; serine proteinase
F:41-118/Domain: kringle homology <KR4>

Query Match 77.8%; Score 407; DB 2; Length 123;
Best Local Similarity 79.3%; Pred. No. 1.1e-34;
Matches 65; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 ROCYHNGOSYRGFTSTVTGRTCSQSWSMTPRHQRTPENYNDGLTMNYCRNPADTG 61

DB 39 QDCYHNGOSYRGFTSTVTGRTCSQSWSMTPRHQRTPENYNDGLTMNYCRNPADTG 98

QY 62 PWCFTTDPISIRWEYCNLTRCSD 83
DB 99 PWCYTTDPISIRWEYCNLTRCSD 120

RESULT 8

plasma (EC 3.4.21.7) precursor - pig (fragment)
N:Alternate names: plasminogen
N:Contains: miniplasminogen
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C/Accession: S03733; S03737; A25834
R/Schaller, J.; Marti, T.; Koessele, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A>Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the car
A/Reference number: S03733
A/Accession: S03733
A/Molecule type: protein
A/Residues: 1-360 <SCH>
R/Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBR fragments of human, l
A/Reference number: S03735; MUID:81212097; PMID:7236497
A/Accession: S03737
A/Molecule type: protein
A/Residues: 1-57 <BRU>
R/Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A>Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A/Reference number: A25834; MUID:85203907; PMID:3846533
A/Accession: A25834
A/Molecule type: protein
A/Residues: 450-790 <MAR>
C/Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a v
us the walls of the graafian follicle; also activates the urokinase-type plasminogen acti
A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C/Keywords: fibrinolysis; glycoprotein; hydrolyase; kidney; kringle; plasma; serine prote
F:1-790/Product: plasminogen #status predicted <PRO>
F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F:1-77/Domain: activation peptide #status predicted <AP>
F:78-560/Product: plasmin chain A #status predicted <ACH>
F:84-162/Domain: kringle homology <KR1>
F:166-243/Domain: kringle homology <KR2>
F:256-333/Domain: kringle homology <KR3>
F:358-435/Domain: kringle homology <KR4>
F:450-790/Product: miniplasminogen #status experimental <MTN>
F:461-540/Domain: kringle homology <KR5>
F:561-790/Product: plasmin chain B #status experimental <BCH>
F:561-783/Domain: trypsin homology <TRY>
F:30-5434-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305-
bonds: #status predicted
F:602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 76.7%; Score 401; DB 1; Length 790;
Best Local Similarity 73.6%; Pred. No. 2.8e-33;
Matches 64; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 ROCYHNGOSYRGFTSTVTGRTCSQSWSMTPRHQRTPENYNDGLTMNYCRNPADTG 61
DB 356 QDCYHNGOSYRGFTSTVTGRTCSQSWSMTPRHQRTPENYNDGLTMNYCRNPADTG 415
QY 62 PWCFTTDPISIRWEYCNLTRCSDT 88
DB 416 PWCYTTDPISIRWEYCNLTRCSDT 442

RESULT 9

PLMS

Plasmin (EC 3.4.21.7) precursor - mouse

N/Contains: angiotensin, plasminogen

C/Species: Mus musculus (house mouse)

C/Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999

C/Accession: A38514; S48202; S48203

R/Begun, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.

Genomics 8, 49-61, 1990

A/Title: Characterization of the cDNA coding for mouse plasminogen and localization of

A/Reference number: A38514; MUID:9184812; PMID:2081600

A/Accession: A38514

A/Molecule type: mRNA

A/Residues: 1-812 <DEG>

A/Cross-references: GB:J04766; NID:G200402; PIDN:AAA50168.1; PID:G200403

R/Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.

Eur. J. Biochem. 224, 863-871, 1994

A/Title: Characterization of the murine plasma fibrinolytic system.

A/Reference number: S48202; MUID:95010076; PMID:7523120

A/Accession: S48202

A/Molecule type: protein

A/Residues: 20-25 <LIJ>

A/Accession: S48203

A/Molecule type: protein

A/Residues: 22-27 <LI2>

C/Comment: Plasminogen is synthesized by the kidney and is present in plasma and many of

C/Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C/Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

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C/Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

plasmin (EC 3.4.21.7) precursor - western European hedgehog

C/Species: Erinaceus europaeus (western European hedgehog)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999

C/Accession: I46260

R/Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong,

J. Biol. Chem. 270, 24004-24009, 1995

A/Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein

A/Reference number: I46259; MUID:96025778; PMID:7592597

A/Accession: I46260

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-810 <LAW>

A/Cross-references: EMBL:U33171; NID:G1046360; PID:G1046361

C/Suprafamily: plasmin, kringle homology; plasminogen-related protein precursor homology;

C/Keywords: hydrolase; serine proteinase

F1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F1-103-181/Domain: kringle homology <KR1>

F1-185-262/Domain: kringle homology <KR2>

F1-275-352/Domain: kringle homology <KR3>

F1-379-456/Domain: kringle homology <KR4>

F1-482-561/Domain: kringle homology <KR5>

F1-582-803/Domain: trypsin homology <TRY>

F1-582-803/Domain: trypsin homology <TRY>

F1-582-803/Domain: trypsin homology <TRY>

F1-582-803/Domain: trypsin homology <TRY>

F1-582-803/Domain: trypsin homology <TRY>

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F1-582-803/Domain: trypsin homology <TRY>

F1-582-803/Domain: trypsin homology <TRY>

plasmin (EC 3.4.21.7) precursor - sheep (fragments)

N/Alternate names: plasminogen

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999

C/Accession: B61545; S28200

R/Schaller, J.; Rickli, E.E.

Enzyme 40, 63-69, 1988

A/Title: Structural aspects of the plasminogen of various species.

A/Reference number: A61545; MUID:89005015; PMID:3168975

A/Accession: B61545

A/Molecule type: protein

A/Residues: 1-37;38-117 <SCH>

R/Schaller, J.; Strub, C.; Kaempfer, U.; Rickli, E.E.

Protein Seq. Data Anal. 5, 21-25, 1992

A/Title: Complete amino acid sequence of ovine miniplasminogen.

A/Reference number: S28200; MUID:93149955; PMID:1492092

A/Accession: S28200

A/Molecule type: protein

A/Residues: 118-460 <SC2>

C/Suprafamily: plasmin, kringle homology; plasminogen-related protein precursor homology;

C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase;

F1-37-38-117/Domain: plasminogen (fragments) #status experimental <PRO>

F1-137/Domain: activation peptide (fragment) #status experimental <APT>

F1-38-117/Domain: activation peptide (fragment) #status experimental <APT>

F1-118-230/Domain: plasmin (fragments) #status experimental <MIN>

F1-118-230/Domain: plasmin (fragments) #status experimental <MIN>

F1-118-230/Domain: plasmin (fragments) #status experimental <MIN>

F1-118-230/Domain: plasmin (fragments) #status experimental <MIN>

F1-118-230/Domain: plasmin (fragments) #status experimental <MIN>

F1-118-230/Domain: plasmin (fragments) #status experimental <MIN>

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F1-118-230/Domain: plasmin (fragments) #status experimental <MIN>

F1-118-230/Domain: plasmin (fragments) #status experimental <MIN>

F1-118-230/Domain: plasmin (fragments) #status experimental <MIN>

[illegible]

F:126-205/Domain: kringle homology <KR5>
F:226-455/Domain: plasmin chain B #status experimental <BCH>
F:226-448/Domain: trypsin homology <TRY>
F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 72.7%; Score 380; DB 2; Length 455;
Best Local Similarity 72.6%; Pred. No. 2,3e-31;
Matches 61; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Oy 1 VRQCTHGNGSYRGFTSTVTGRTCSWSSMTPHRHQRTPEYNDGLTMNYCRNPADPT 60
Db 34 VQDCYQDGBSEYRGFTSTVTGKCCQSWSSMTPHMHQKTPKXPYNDGLTMNYCRNPDGDK 93
Oy 61 GPMCFETDPSIRMEYCNLTTRCSDT 84
Db 94 GPMCFETDPSVMEYCNLTTRCSET 117

RESULT 14
A:60140
Plasmin (BC 3.4.21.7) precursor - chicken (fragment)
N:Alternate names: plasminogen
C:Species: Gallus gallus (chicken)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
C:Accession: A60140
R:Gene(s), M., Patchy, L.
Biochim. Biophys. Acta 832, 326-330, 1985
A:Title: The kringle 4 domain of chicken plasminogen.
A:Reference number: A60140; MUID:86077796; PMID:4074753
A:Accession: A60140
A:Molecule type: protein
A:Residues: 1-89 <GR>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F:6-83/Domain: kringle homology <KR>
F:6-83,27-66,55-78/Disulfide bonds: #status predicted
F:39/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 67.7%; Score 354; DB 2; Length 89;
Best Local Similarity 67.9%; Pred. No. 2.1e-29;
Matches 55; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Oy 3 QCYHNGSYRGFTSTVTGRTCSWSSMTPHRHQRTPEYNDGLTMNYCRNPADPTGP 62
Db 5 ECVGNGSYRGFTSTVTGKCCQSWSSMTPHRHQRTPEYNDGLTMNYCRNPADPTDRSP 64
Oy 63 WCFTTDPSPIRMEYCNLTTRCSD 83
Db 65 WCFTTDPSPVMEYCNLTTRCSD 85

RESULT 15
T18518
Apolipoprotein(a) - western European hedgehog (fragment)
C:Species: Erinaceus europaeus (western European hedgehog)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C:Accession: T18518
R:Lawn, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong,
J. Biol. Chem. 270, 24004-24009, 1995
A:Title: The recurring evolution of lip(a): Insights from cloning of hedgehog apolipoprotein
A:Reference number: 146259; MUID:96025778; PMID:7592597
A:Accession: T18518
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2869 <LAW>
A:Cross-references: EMBL:U33170; NID:g1046358; PID:g1046359; PIDN:AA048522.1
A:Experimental source: liver
C:Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con-

Query Match 57.9%; Score 303; DB 2; Length 2869;
Best Local Similarity 56.2%; Pred. No. 1.1e-22;
Matches 46; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 3 QCVHNGOSYRGTFESTTVTGRTCOSWSMTPHRHORTPENYPNDGLTMNYCRUPADTGP 62
 DB 2776 QCLKNGESTQGNISVTSGYTCORNRBOTPHRHARTPDNYPCKNLVGNICRNPDSGVAP 2835
 QY 63 WCFETDPSIRWEXCNLTRC 81
 DB 2836 WCYTNSAVRWEXCSIPTC 2854

Search completed: January 12, 2004, 17:26:24
 Job time : 13.0451 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:17:22 ; Search time 7.69549 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-10-088-548-6
Sequence: 1 VRQCHNGNSYRGFTSTV.....SIRWEXNLTGRCSDTEGTIV 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	98.9	4548	1 APOA_HUMAN	P08519 homo sapien
2	478	91.4	1420	1 APOA_MACMU	P14417 macaca mula
3	444	84.9	810	1 PLMN_HUMAN	P00747 homo sapien
4	433	82.8	810	1 PLMN_MACMU	P12545 macaca mula
5	435	79.3	812	1 PLMN_BOVIN	P06868 bos taurus
6	401	76.7	790	1 PLMN_PIG	P06867 sus scrofa
7	400	76.5	812	1 PLMN_MOUSE	P20918 mus musculu
8	392	75.0	169	1 PLMN_ERIEU	Q29485 erinaceus e
9	381.5	72.9	169	1 PLMN_RAT	Q01177 rattus norv
10	272.5	52.1	716	1 HGF_MOUSE	P26928 mus musculu
11	269	51.4	728	1 HGF_HUMAN	P14210 homo sapien
12	263	50.3	728	1 HGF_MOUSE	Q08048 mus musculu
13	263	50.3	728	1 HGF_RAT	P17945 rattus norv
14	247.5	47.3	711	1 HGF_HUMAN	P26927 mus musculu
15	234	44.7	343	1 PLMN_SHEEP	P81286 ovie aries
16	233	44.6	333	1 PLMN_CANFA	P80009 canis fami
17	222	42.4	338	1 PLMN_HORSE	P80010 equus cabal
18	216.5	41.4	943	1 ROR_HUMAN	Q01974 homo sapien
19	208.5	39.9	944	1 ROR_MOUSE	Q92138 mus musculu
20	205	39.2	325	1 PLMN_PETMA	P33574 petromyzon
21	204.5	39.1	622	1 THRE_HUMAN	P00734 homo sapien
22	204	39.0	625	1 THRE_BOVIN	P00735 bos taurus
23	201.5	38.5	617	1 THRE_RAT	P18392 rattus norv
24	199.5	38.1	618	1 THRE_MOUSE	P19221 mus musculu
25	193.5	37.0	603	1 FA12_CAVPO	Q04962 cavia porce
26	192.5	36.8	937	1 ROR_MOUSE	Q92139 mus musculu
27	191.5	36.6	937	1 ROR_HUMAN	Q01973 homo sapien
28	189	36.1	562	1 TPA_HUMAN	P00750 homo sapien
29	188.5	36.0	615	1 FA12_HUMAN	P00748 homo sapien
30	187.5	35.9	724	1 ROR2_DROME	Q956K3 drosophila
31	182	34.8	566	1 TPA_BOVIN	Q92198 bos taurus
32	174	33.3	653	1 HGF_MOUSE	Q92098 mus musculu
33	173	33.1	559	1 TPA_MOUSE	P11214 mus musculu

34	173	33.1	559	1 TPA_RAT	P19637 rattus norv
35	171.5	32.8	452	1 UROK_RAT	P29598 rattus norv
36	170	32.5	631	1 HGF_HUMAN	Q04756 homo sapien
37	167.5	32.0	473	1 KRM1_MOUSE	Q99N43 mus musculu
38	167.5	32.0	473	1 KRM1_RAT	Q92484 mus musculu
39	166.5	31.8	593	1 FA12_BOVIN	P98140 bos taurus
40	164.5	31.5	475	1 KRM1_HUMAN	Q96mu8 homo sapien
41	163.5	31.3	452	1 KRM1_XENLA	Q90Y90 xenopus lae
42	160	30.6	433	1 UROK_PAPCY	P16227 papio cynoc
43	159	30.4	431	1 UROK_DESRO	P98121 desmodus ro
44	159	30.4	462	1 KRM2_HUMAN	Q8ncw0 homo sapien
45	159	30.4	477	1 URT2_DESRO	P15638 desmodus ro

ALIGNMENTS

RESULT 1
ID APOA_HUMAN STANDARD: PRT: 4548 AA.
AC P08519:
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
GN LPA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88039109; PubMed=3670400;
RA McLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
RT Fless G.M., Scam A.M., Lawn R.M.;
RT "CDNA sequence of human apolipoprotein(a) is homologous to
RT plasminogen.";
RL Nature 330:132-137(1987).
RN [2]
RP SERINE PROTEASE ACTIVITY.
RX MEDLINE=90076123; PubMed=2531657;
RA Salonen E.-M., Jauhainen M., Zairi L., Vaheri A., Ehnholm C.;
RT "Lipoprotein(a) binds to fibronectin and has serine proteinase
RT activity capable of cleaving it.";
RL EMBO J. 8:4035-4040(1989).
RN [3]
RP REVIEW.
RX MEDLINE=90049223; PubMed=2530631;
RA Utermann G.;
RT "The mysteries of lipoprotein(a).";
RL Science 246:904-910(1989).
RN [4]
RP CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
RX MEDLINE=2103595; PubMed=11294842;
RA Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
RT "Structural elucidation of the N- and O-glycans in conferring protease
RT resistance.";
RL J. Biol. Chem. 276:22200-22208(2001).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
RX MEDLINE=96217891; PubMed=8642595;
RA Mikol V., Lograsse P.V., Beutcher B.R.;
RT "Crystal structures of apolipoprotein(a) kingle IV37 free and
RT complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
RT acid: existence of novel and expected binding modes.";
RL J. Mol. Biol. 256:751-761(1996).
RN [6]
RP VARIANT ARG-4193.
RX MEDLINE=95002201; PubMed=7918682;
RA Scam A.M., Pfaffinger D., Lee J.C., Himman J.;
RT "A single point mutation (Trp72->Arg) in human apo(a) kingle 4-37
RT associated with a lysine binding defect in Lp(a).";

```

RL BLOCINB Biophys. Acta 1227:41-45(1994) .
CC -I- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
CC      (Lp(a)). It has serine protease activity and is able of
CC      autoprotoeolysis. Inhibits tissue-type plasminogen activator 1.
CC      Lp(a) may be a ligand for megalin/GP 330.
CC -I- SUBUNIT: disulfide-linked to apo-B100. Binds to fibronectin and
CC      decorin.
CC -I- PTM: N- and O-glycosylated. The N-glycans are complex biantennary
CC      structures present in either a mono- or distallylated state. The
CC      O-glycans are mostly (80%) represented by the monosialylated core
CC      type-I structure, NeuNAcalpha6-2-3Galbeta1-3GalNac, with smaller
CC      amounts of distalylated and non-siallylated O-glycans also
CC      detected.
CC -I- DISEASE: Elevated plasma concentrations of apo(a) and its
CC      naturally occurring procoagolytic fragments are correlated with
CC      atherosclerosis. Homology with plasminogen kringle IV and V is
CC      thought to underlie the atherogenicity of the protein, because the
CC      fragments are competing with plasminogen for fibrin(ogen) binding.
CC -I- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
CC      leading to the formation of the so called mini-Lp(a). Apo(a)
CC      fragments accumulate in atherosclerotic lesions, where they may
CC      promote thrombogenesis. O-glycosylation may limit the extent of
CC      proteolytic fragmentation.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -I- SIMILARITY: Contains 38 kringle domains.
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CC or send an email to license@isb.slb.ch) .
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DR EMBL; X06290; CAA29618.1; -.
DR PIR; S00657; S00657.
DR PDB; 117J; 13-JUN-01.
DR PDB; 1JFN; 28-JUN-02.
DR PDB; 3KIV; 18-MAY-99.
DR PDB; 3KIV; 18-MAY-99.
DR PDB; 4KIV; 18-MAY-99.
DR MEROPS; S01.226; -.
DR Genew; HGNC:6667; LPA.
DR MIM; 152200; -.
DR GO; GO:0004866; F:endopeptidase inhibitor activity; TAS.
DR GO; GO:0008015; P:circulation; TAS.
DR GO; GO:0009405; P:pathogenesis; TAS.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle_38.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle_38.
DR SMART; SM00130; KR; 38.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 38.
DR PROSITE; PSS0070; KRINGLE_2; 38.
DR PROSITE; PSS0240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00133; TRYPsin_SER; 1.
KM Hydroxylase; Serine peptidase; Lipid transport; Plasma; Glycoprotein;
FM Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3d-structure.
FT SIGNAL                     1          19
FT CHAIN                      20         4548
FT DOMAIN                    20         130    APOLIPOPROTEIN(A) .
FT DOMAIN                   131        244    KRINGLE TYPE IV, 1.
FT DOMAIN                   245        358    KRINGLE TYPE IV, 2.
FT DOMAIN                   359        472    KRINGLE TYPE IV, 3.
FT DOMAIN                   473        586    KRINGLE TYPE IV, 4.
FT DOMAIN                   587        700    KRINGLE TYPE IV, 5.
FT DOMAIN                   701        814    KRINGLE TYPE IV, 6.
FT DOMAIN                   701        814    KRINGLE TYPE IV, 7.

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FT	DOMAIN	815	928		KRINGLE TYPE IV, 8.
FT	DOMAIN	929	1042		KRINGLE TYPE IV, 9.
FT	DOMAIN	1043	1156		KRINGLE TYPE IV, 10.
FT	DOMAIN	1157	1270		KRINGLE TYPE IV, 11.
FT	DOMAIN	1271	1384		KRINGLE TYPE IV, 12.
FT	DOMAIN	1385	1498		KRINGLE TYPE IV, 13.
FT	DOMAIN	1499	1612		KRINGLE TYPE IV, 14.
FT	DOMAIN	1613	1726		KRINGLE TYPE IV, 15.
FT	DOMAIN	1727	1840		KRINGLE TYPE IV, 16.
FT	DOMAIN	1841	1954		KRINGLE TYPE IV, 17.
FT	DOMAIN	1955	2068		KRINGLE TYPE IV, 18.
FT	DOMAIN	2069	2182		KRINGLE TYPE IV, 19.
FT	DOMAIN	2183	2296		KRINGLE TYPE IV, 20.
FT	DOMAIN	2297	2410		KRINGLE TYPE IV, 21.
FT	DOMAIN	2411	2524		KRINGLE TYPE IV, 22.
FT	DOMAIN	2525	2638		KRINGLE TYPE IV, 23.
FT	DOMAIN	2639	2752		KRINGLE TYPE IV, 24.
FT	DOMAIN	2753	2866		KRINGLE TYPE IV, 25.
FT	DOMAIN	2867	2980		KRINGLE TYPE IV, 26.
FT	DOMAIN	2981	3094		KRINGLE TYPE IV, 27.
FT	DOMAIN	3095	3208		KRINGLE TYPE IV, 28.
FT	DOMAIN	3209	3322		KRINGLE TYPE IV, 29.
FT	DOMAIN	3323	3436		KRINGLE TYPE IV, 30.
FT	DOMAIN	3437	3550		KRINGLE TYPE IV, 31.
FT	DOMAIN	3551	3664		KRINGLE TYPE IV, 32.
FT	DOMAIN	3665	3770		KRINGLE TYPE IV, 33.
FT	DOMAIN	3771	3884		KRINGLE TYPE IV, 34.
FT	DOMAIN	3885	3998		KRINGLE TYPE IV, 35.
FT	DOMAIN	3999	4112		KRINGLE TYPE IV, 36.
FT	DOMAIN	4113	4226		KRINGLE TYPE V.
FT	DOMAIN	4227	4327		SERINE PROTEASE.
FT	DOMAIN	4328	4548		CHARGE RELAY SYSTEM.
FT	ACT_SITE	4369	4369		CHARGE RELAY SYSTEM.
FT	ACT_SITE	4412	4412		CHARGE RELAY SYSTEM.
FT	ACT_SITE	4498	4498		W -> R (LOSS OF LYSINE-SEPHAROSE BINDING).
FT	VARIANT	4193	4193		/FtId=VAR_006633.
SO	SEQUENCE	4548 AA;	501313 MM;	96921BE96A465C5F CRC64;	
	Query Match		98.9%;	Score 517; DB 1; Length 4548;	
	Best Local Similarity		98.9%;	Pred. No. 4.1e-47;	
	Matches	88;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
Oy	1 VRQCIHNGGOSYKRGTFSTTVTGRTCGSSMTPIRRHQTPENPNNDGLTMNYCRNPADT	60			
Db	4121 VRQCYHNGGOSYKRGTFSTTVYGRTCGSSMTPIRRHQTPENPNNDGLTMNYCRNPADT	4180			
Oy	61 GPWCFTDPSIRWEYCNLTRCSDEGTIV	89			
Db	4181 GPWCFTMDPSIRWEYCNLTRCSDEGTIV	4209			
	RESULT 2				
ID	_APOA_MACMU	STANDARD;	PRT:	1420 AA.	
AC	P14417;				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Apolipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment).				
GN	LpA.				
OS	Macaca mulatta (Rhesus macaque).				
OC	Mammalia; Metazoa; Chordata; Ctenidiata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;				
OC	Cercopithecinae; Macaca.				
OX	NCBI_TaxID=9544;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89174660; PubMed=2925643;				
RA	Tomlinson J.E., McLean J.W., Lawn R.M.;				
RT	"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis."				

RT "The primary structure of human plasminogen. II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence."
RL J. Biol. Chem. 248:1631-1633(1973).
RN [10]
RP ACTIVE SITE.
RX MEDLINE=69234739; PubMed=4240117;
RT Groshkopf W.R., Summaria L., Robbins K.C.;
RA "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue."
RL J. Biol. Chem. 244:3590-3597(1969).
RN [11]
RX OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RP MEDLINE=82213905; PubMed=6919539;
RA Trexler M., Vail Z., Patchy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringle 4."
RL J. Biol. Chem. 257:7401-7406(1982).
RN [12]
RP FTBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE=85054794; PubMed=6094526;
RA Vail Z., Patchy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringle 1 domain."
RL J. Biol. Chem. 259:13690-13694(1984).
RN [13]
RX PHOSPHORYLATION SITE SER-597.
RP MEDLINE=97345939; PubMed=9201958;
RA Wang H., Proxok M., Bretthauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen."
RL Biochemistry 36:8100-8106(1997).
RN [14]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kameiling J.P.,
RA Gerwig G.J., van Halbeek H., Vlieghart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns."
RL Eur. J. Biochem. 173:57-63(1988).
RN [15]
RP CARBOHYDRATE-LINKAGE SITE SER-268.
RX MEDLINE=97207306; PubMed=9054441;
RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RA Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated triaccharide on Ser-248 of
RT human plasminogen 2."
RL J. Biol. Chem. 272:7408-7411(1997).
RN [16]
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenchal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma."
RL Cell 79:315-328(1994).
RN [17]
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=97238710; PubMed=9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
RA Lapcevic R., Nagy C.A.;
RT "A recombinant human angiotensin protein inhibits experimental primary
RT and metastatic cancer."
RL Cancer Res. 57:1329-1334(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=92031502; PubMed=1657148;
RA Mullick A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
RT refined at 1.9-A resolution."
RL Biochemistry 30:10576-10588(1991).
RN [19]

RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=92031503; PubMed=1657149;
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mullick A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringle 4."
RL Biochemistry 30:10589-10594(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RA Stec B., Yamano A., Whitlow M., Teeter M.M.;
RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
RT A possible structural role of disordered residues."
RL Acta Crystallogr. D 53:169-178(1997).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE=96180681; PubMed=8611560;
RA Mathews I.I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringle 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid."
RL Biochemistry 35:2567-2576(1996).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE=98198034; PubMed=9521645;
RA Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringle
RT 5 domain of human plasminogen."
RL Biochemistry 37:3258-3271(1998).
RN [23]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237157; PubMed=8181475;
RA Rejzante M.R., Llinas M.;
RT "1H-NMR assignments and secondary structure of human plasminogen
RT kringle 1."
RL Eur. J. Biochem. 221:927-937(1994).
RN [24]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237158; PubMed=8181476;
RA Rejzante M.R., Llinas M.;
RT "Solution structure of the epsilon-aminohexanoic acid complex of
RT human plasminogen kringle 1."
RL Eur. J. Biochem. 221:939-949(1994).
RN [25]
RP STRUCTURE BY NMR OF 183-354.
RX MEDLINE=96194156; PubMed=8652577;
RA Seehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
RA Rickli E.E.;
RT "Recombinant gene expression and 1H NMR characteristics of the
RT kringle (2 + 3) supermodule: spectroscopic/functional individuality
RT of plasminogen kringle domains."
RL Biochemistry 35:2357-2364(1996).
RN [26]
RP STRUCTURE BY NMR OF 374-461.
RX MEDLINE=90219023; PubMed=2157850;
RA Atkinson R.A., Williams R.J.P.;
RT "Solution structure of the kringle 4 domain from human plasminogen by
RT 1H nuclear magnetic resonance spectroscopy and distance geometry."
RL J. Mol. Biol. 212:541-552(1990).
RN [27]
RP VARIANTS PHE-374 AND THR-620.
Query Match 84.9%; Score 444; DB 1; Length 810;
Best Local Similarity 82.0%; Pred. No. 4,3e-40;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

RESULT 4
PLMN MACMU
ID PLMN MACMU STANDARD; PRT; 810 AA.
AC P12545;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
GN PLG.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89174660; PubMed=2925643;
RA Tomlinson J.E., McLean J.W., Lawn R.M.;
RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
synthesis";
RL J. Biol. Chem. 264:5957-5965(1989).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa;
higher selectivity than trypsin. Converts fibrin into soluble
products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STEPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD
TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: contains 5 kringle domains.
CC -----
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or send an email to license@isb-sib.ch).
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DR EMBL; J04697; AAA36901.1; -
DR PIR; B32869; B30848.
DR HSSP; P00747; 1PMK.
DR MEROPS; S01.233;
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; PAN_APP.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00021; KRINGLE 1; 5.
DR PROSITE; PS50070; KRINGLE 2; 5.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase, Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 184 262 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 377 454 KRINGLE 4.
FT DOMAIN 481 560 KRINGLE 5.
FT DOMAIN 581 810 SERINE PROTEASE.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 655 655 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 158 158 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 432 432 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 134 134 FIBRIN.
FT BINDING 136 136 FIBRIN.
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 61 BY SIMILARITY.
FT DISULFID 103 181 BY SIMILARITY.
FT DISULFID 124 164 BY SIMILARITY.
FT DISULFID 152 176 BY SIMILARITY.
FT DISULFID 185 262 BY SIMILARITY.
FT DISULFID 188 316 BY SIMILARITY.
FT DISULFID 206 245 BY SIMILARITY.
FT DISULFID 234 257 BY SIMILARITY.
FT DISULFID 275 352 BY SIMILARITY.
FT DISULFID 296 335 BY SIMILARITY.
FT DISULFID 324 347 BY SIMILARITY.
FT DISULFID 377 454 BY SIMILARITY.
FT DISULFID 398 437 BY SIMILARITY.
FT DISULFID 426 449 BY SIMILARITY.
FT DISULFID 481 560 BY SIMILARITY.
FT DISULFID 502 543 BY SIMILARITY.
FT DISULFID 531 585 BY SIMILARITY.
FT DISULFID 567 685 BY SIMILARITY.
FT DISULFID 577 585 BY SIMILARITY.
FT DISULFID 607 623 BY SIMILARITY.
FT DISULFID 699 766 BY SIMILARITY.
FT DISULFID 729 745 BY SIMILARITY.
FT DISULFID 756 784 BY SIMILARITY.
FT CARBOHYD 365 365 O-LINKED (GLNAC...) (BY SIMILARITY).
SQ SEQUENCE 810 AA; 90255 MW; A75E1C51A0B224A CXC64;
Query Match 82.8%; Score 433; DB 1; Length 810;
Best Local Similarity 79.5%; Pred. No. 6.5e-39;
Matches 70; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
QY 1 VROCCHNGSGSYRGFTTGTGRTQSSSMTPHRHQTPENYPDGLTMNYCRPPADDT 60
DB 374 VQECTHGSGSYRGFTTGTGRTQSSSMTPHRHQTPENYPDGLTMNYCRPPADDT 433
QY 61 GPWCFTTDPSSIRWEXCNLTRCSDEGTGTV 88
DB 434 GPWCFTTDPSSIRWEXCNLTRCSDEGTGTV 461
RESULT 5
PLMN BOVIN
ID PLMN BOVIN STANDARD; PRT; 812 AA.

AC P06868; Q28162; 01-JAN-1998 (Rel. 06, Created)
 DT 01-JAN-1998 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7).
 GN PLG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Berglund L., Andersen M.D., Petersen T.E.;
 RT Cloning and characterization of the bovine plasminogen cDNA.;
 RL Int. Dairy J. 5:593-603(1995).
 RN [2]
 RP SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=85203906; Pubmed=3846532;
 RA Schaller J., Moser P.W., Danneberger-Muller G.A.K., Rosselet S.J.,
 RA Kamper U., Rickli E.E.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with
 human plasminogen.";
 RL Eur. J. Biochem. 149:267-278(1985).
 RN [3]
 RP SEQUENCE OF 706-812 FROM N.A.
 RX MEDLINE=85023311; Pubmed=614961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 human and bovine plasminogen.";
 RL Biochemistry 23:4243-4250(1984).
 RN [4]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; Pubmed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kameiling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 plasminogen. Species specificity in relation to sialylation and
 fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 RN [5]
 RP FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
 GLAFLITAN FOLLICLE. IT ACTIVATES THE UKONINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC PTM: N-LINKED GLYCAN CONTAIN N-ACETYLACTOSAMINE AND STATIC ACID.
 CC O-LINKED GLYCANS CONSIST OF GAL-GALNAc DISACCHARIDE WITH IS
 MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
 CC MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC SIMILARITY: Contains 5 kringle domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 or send an email to license@ebi.ac.uk).
 CC EMBL; X79402; CAA55939.1; -
 CC EMBL; K02935; AAA30714.1; -

DR PIR; S45046; PLBO.
 DR HSSP; P00747; 2PK4.
 DR MEROPS; S01.233; -
 DR GlycoSuiteDB; P06868; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan. app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00051; kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS50070; KRINGLE_2; 5.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 DR Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KM Signal.
 FT SIGNAL. 1 26
 FT CHAIN 27 812 PLASMINOGEN.
 FT CHAIN 27 583 PLASMIN HEAVY CHAIN A.
 FT CHAIN 584 812 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 110 188 KRINGLE 1.
 FT DOMAIN 192 269 KRINGLE 2.
 FT DOMAIN 282 359 KRINGLE 3.
 FT DOMAIN 384 461 KRINGLE 4.
 FT DOMAIN 485 564 KRINGLE 5.
 FT DOMAIN 584 812 SERINE PROTEASE.
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 365 365 O-LINKED (GALNAc. . .)
 FT ACT SITE 624 624 /FTID=CAR_000015.
 FT ACT SITE 667 667 CHARGE RELAY SYSTEM.
 FT ACT SITE 762 762 CHARGE RELAY SYSTEM.
 FT CONFLICT 335 335 N -> D (IN REF. 2).
 FT CONFLICT 516 516 Q -> H (IN REF. 2).
 FT CONFLICT 555 555 P -> L (IN REF. 2).
 FT CONFLICT 744 744 T -> R (IN REF. 3).
 SQ SEQUENCE 812 AA; 91216 MW; 38A6A691E220946 CRC64;
 Query Match 79.3%; Score 415; DB 1; Length 812;
 Best Local Similarity 79.5%; Pred. No. 5.5e-17;
 Matches 66; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
 QY 2 RQCYHNGOSYRSTFTVYGRTCQSSWTPRHQRTPENYNDGLTNNYCNPNADTG 61
 DB 382 QDCYHNGOSYRSTFTVYGRTCQSSWTPRHRLKTEBNYDAGLTNNYCNPNADKS 441
 QY 62 PWCFTTDPSTIRWEYCNLTCSDT 84
 DB 442 PWCYTTDPVRFWEFCNLKCKSET 464
 RESULT 6
 PLNM_PIG STANDARD; PRT; 790 AA.
 AC P06867;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen (EC 3.4.21.7).
 GN PLG.

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE OF 1-560.
 RA Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli E.E.;
 RT "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
 of the carbohydrate attachment sites with the human and bovine
 species.";
 RL Fibrinolysis 1:91-102(1987).
 RN [2]
 RP SEQUENCE OF 450-790.
 RX MEDLINE=85203907; PubMed=3846533;
 RA Marti T., Schaller J., Rickli E.E.;
 RT "Determination of the complete amino-acid sequence of porcine
 miniplasminogen.";
 RL Eur. J. Biochem. 149:279-285(1985).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 plasminogen. Species specificity in relation to sialylation and
 fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 GRAAFIAN FOLLICLE, IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOSINS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCAN CONTAINS N-ACETYLACTOSAMINE, SIALIC ACID AND
 IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAc
 DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
 (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALFHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC PIR: S03733; PIRG.
 DR HSP: P00747; SHPG.
 DR MEROPS: S01.233; -.
 DR GLYCOSULEDB: P06867; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser protease_Try.
 DR Pfam: PF00051; kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 5.
 DR SMART: SM00130; KR; 5.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.

DR PROSITE, PS00135; TRYPSIN_SER; 1.
 KM Hydroxylase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 RN Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
 FT CHAIN 1 560 PLASMIN HEAVY CHAIN A.
 FT CHAIN 561 790 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 561 790 SERINE PROTEASE.
 FT DOMAIN 84 162 KRINGLE 1.
 FT DOMAIN 166 243 KRINGLE 2.
 FT DOMAIN 256 333 KRINGLE 3.
 FT DOMAIN 358 435 KRINGLE 4.
 FT DOMAIN 461 540 KRINGLE 5.
 FT ACT_SITE 602 602 CHARGE RELAY SYSTEM.
 FT ACT_SITE 645 645 CHARGE RELAY SYSTEM.
 FT ACT_SITE 740 740 CHARGE RELAY SYSTEM.
 FT CARBOHYD 289 289 N-LINKED (GLCNAc. . .).
 FT CARBOHYD 340 340 /FTid=CAR_000019.
 FT CARBOHYD 340 340 /FTid=CAR_000020.
 FT CARBOHYD 340 340 /FTid=CAR_000020.
 SQ SEQUENCE 790 AA; 88592 MM; F04EAD0674BCD58E CRC64;
 Query Match 76.7%; Score 401; DB 1; Length 790;
 Best Local Similarity 73.6%; Pred. No. 1.7e-35;
 Matches 64; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 QY 2 RQCYHNGQSYRGFTSTVTGTCQSSSWTPHRHQRTPEPNYDGLTMYCRNPDADTG 61
 DB 356 QDCYRNGESYRGFTSTVTGTCQSSSWTPHRHQRTPEPNYDGLTMYCRNPDADTG 61
 QY 62 FWCFTTDPDSIMRYCNLTGCSDTGTV 88
 DB 416 FWCYTTDPDRVWEYCNLKCSETEQV 442
 RESULT 7
 PLMN_MOUSE STANDARD; PRT; 812 AA.
 ID P20918; Q8C182; Q91WU5;
 AC 01-FEB-1991 (Rel. 17, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
 GN PLG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184812; PubMed=2081600;
 RA Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
 RT "Characterization of the cDNA coding for mouse plasminogen and
 localization of the gene to mouse chromosome 17.";
 RL Genomics 8:49-61(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv.
 RA Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schleisinger D.,
 Nagelraja R.;
 RT "Genomic sequence analysis in the mouse t-complex region.";
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ueidi T.B., Toshimaki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
SEQUENCE OF 1-16 FROM N.A.
RC STRAIN=129/8v; TISSUE=Liver;
RX PubMed=12149246;
RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA Farmer R.J., Miles L.A.,
RT "Localization of regulatory elements mediating constitutive and
RT cytokine-stimulated plasminogen gene expression.";
J. Biol. Chem. 277:38579-38588(2002).
[5]
CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage B.H., Folkman J.,
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
Cell 79:315-328(1994).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
CC NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
CC METASTATIC TUMORS IN VIVO.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
CC INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringe domains.
CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: J04766; AA50168.1; -;
CC EMBL: AF481053; AA022156.1; -;
CC EMBL: BC014773; AA014773.1; -;
CC EMBL: AY134430; AA015805.1; -;
CC PIR: A38514; PLMS.
CC HSSP: P00747; PLMS.
CC MEROPS: S01.233; -;
CC MCD; MGT:97620; PLG.
CC GO; GO:0016506; F:apoptosis activator activity; IDA.
CC GO; GO:0006915; P:apoptosis; IDA.
CC InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000001; Kringe.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan. app.
DR InterPro; IPR003966; Prochrombin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00051; Kringe; 5.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringe; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp. Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringe; Zymogen; Repeat;
KW Signal.
KW Signal.
FT CHAIN 1 19
FT CHAIN 20 812
FT CHAIN 20 581
FT PEPTIDE 20 97
FT CHAIN 98 581
FT CHAIN 98 7436
FT CHAIN 582 812
FT CHAIN 103 181
FT DOMAIN 184 262
FT DOMAIN 275 352
FT DOMAIN 377 454
FT DOMAIN 481 560
FT DOMAIN 582 812
FT ACT SITE 624 624
FT ACT SITE 667 667
FT ACT SITE 762 762
FT DISULFID 49 73
FT DISULFID 53 61
FT DISULFID 103 181
FT DISULFID 124 164
FT DISULFID 152 176
FT DISULFID 185 262
FT DISULFID 188 316
FT DISULFID 206 245
FT DISULFID 234 257
FT DISULFID 275 352
FT DISULFID 296 335
FT DISULFID 324 347
FT DISULFID 377 454
FT DISULFID 398 437
FT DISULFID 426 449
FT DISULFID 481 560
FT DISULFID 502 543
FT DISULFID 531 555
FT DISULFID 568 687
FT DISULFID 578 586
FT DISULFID 609 625
FT DISULFID 701 768
FT DISULFID 731 747
FT DISULFID 758 786
FT CONFLICT 235 235
FT CONFLICT 525 525
FT CONFLICT 649 649
SQ SEQUENCE 812 AA; 90781 MW; 241732605A2FFD2 CRC64;

Query Match 76.5%; Score 400; DB 1; Length 812;
Best Local Similarity 70.8%; Pred. No. 2,3e-35;
Matches 63; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 1 VROCYHNGQSYKRGFTSTVLTGRTCSWSSMTPHRQRTPEPNYNDGLTMNTCRNPADAT 60


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Db 374 VOECYOSDQSYRGSTSTITTKKCCSWAMAMPRHRSKTPENPDAGLEMYCRNPDGDK 433
QY 61 GPMCFITDPSIRWEXCNLTRCSDETEGV 89
DB 434 GPMCFITDPSIRWEXCNLTRCSDETEGV 462

RESULT 8
PLMN_ERIEU STANDARD; PRT; 810 AA.
AC 029485;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
GN PLG.
OS Etrineus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxId=9365;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96025778; Pubmed=7592597;
RA Lamm R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
RA Byrne C.D., Fong K.J., Meer K., Patchy L.,
RT "The recurring evolution of lipoprotein(a). Insights from cloning of
RT hedgehog apolipoprotein(a).".
RT J. Biol. Chem. 270:24004-24009(1995).
RN [2]
RP REVISIONS.
RA Lamm R.M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UKONINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC
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CC
CC EMBL, U31171; AAC48717.1; -
CC PIR, I46260; I46260.
CC HSSP, P00747; IPMK.
CC
CC MEROPS, S01.233; -
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR001014; PAN.
CC InterPro: IPR003609; Pan_app.
CC InterPro: IPR003966; Prothrombin.
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam, PF00051; kringle_5.
CC Pfam, PF00024; PAN; 1.

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DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00020; KRINGLE_1; 5.
DR PROSITE; PS00021; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolytic;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KM Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
FT DOMAIN 583 810 SERINE PROTEASE.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 185 262 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 379 456 KRINGLE 4.
FT DOMAIN 482 561 KRINGLE 5.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT CARBOHYD 339 339 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 810 AA; 90902 MW; 8E7578046017A16 CRC64;

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Query Match 75.0%; Score 192; DB 1; Length 810;

Best Local Similarity 71.8%; Pred. No. 1.6e-34; Matches 61; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

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QY 1 VOECYOSDQSYRGSTSTITTKKCCSWAMAMPRHRSKTPENPDAGLEMYCRNPDGDK 60
DB 376 VOECYOSDQSYRGSTSTITTKKCCSWAMAMPRHRSKTPENPDAGLEMYCRNPDGDK 435
QY 61 GPMCFITDPSIRWEXCNLTRCSDETEGV 85
DB 436 GPMCFITDPSIRWEXCNLTRCSDETEGV 460

RESULT 9
PLMN_ERIEU STANDARD; PRT; 169 AA.
AC 001177;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN PLG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; Pubmed=1645711;
RA Kanalas J.J., Makler S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen."
RT J. Biol. Chem. 266:10825-10829(1991).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UKONINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,

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CC CC LAMININ AND VON WILLEBRAND FACTOR.
CC CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa;
CC CC higher selectivity than trypsin. Converts fibrin into soluble
CC CC products.
CC CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC CC FIBRIN. CANNOT BE ACTIVATED WITH STEPTOKINASE.
CC CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC CC -1- SIMILARITY: Contains 5 kringle domains.
CC CC -----
CC CC CC THE SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC or send an email to license@isb-sb.ch).
CC CC -----
CC CC EMBL: M62832; AAA41884.1; -.
CC CC PIR: A40522; A40522.
CC CC HSSP: P00747; 1PMK.
CC CC -----
CC CC DR MEROPS: S01.233; -.
CC CC DR InterPro: IPR000001; Kringle.
CC CC DR InterPro: IPR003966; Prothrombin.
CC CC DR InterPro: IPR001254; Ser.protease_Try.
CC CC DR Pfam: PF00051; kringle; 2.
CC CC DR PRINTS: PR00018; KRINGLE.
CC CC DR PRINTS: PR01505; PROTHROMBIN.
CC CC DR ProDom: PD00395; Kringle; 2.
CC CC DR SMART: SM00130; KR; 1.
CC CC DR PROSITE: PS00021; KRINGLE_1; 1.
CC CC DR PROSITE: PS00070; KRINGLE_2; 2.
CC CC DR PROSITE: PS0240; TRYPSIN_DOM; PARTIAL.
CC CC DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
CC CC DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
CC CC KW Hydrolyse: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
CC CC tissue remodeling; Blood coagulation; Kringle; Repeat.
CC CC FT NON_TER 1 1
CC CC FT DOMAIN <1 10 KRINGLE 3 (BY SIMILARITY).
CC CC FT DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
CC CC FT DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
CC CC FT DISULFID 34 112 BY SIMILARITY.
CC CC FT DISULFID 55 95 BY SIMILARITY.
CC CC FT DISULFID 83 107 BY SIMILARITY.
CC CC FT NON_TER 169 169
CC CC SQ SEQUENCE 169 AA; 18401 MW; 77A54214C49D010C CRC64;

Query Match 72.9%; Score 381.5; DB 1; Length 169;
Best Local Similarity 71.9%; Pred. No. 3.9e-34;
Matches 64; Conservative 9; Mismatches 15; Indels 1; Gaps 1.

OY 1 VROCHGNGSQYRGFTFTVTGRTGOSQSSMTPHRHQRTPENYPDNGLTMYNCRPDD- 59
DB 31 VOECQNGKSKRGSSSTTNNGKKQGSVMSPHSHSKTPANFPDGLGEMNYCRAPDDQ 90
OY 60 TGPWCFTTDPSTIRMEYCNLTGCSDEGTV 88
DB 91 RGPWCFTTDPSTIRMEYCNLTGCSDEGTV 119

RESULT 10
HGFL_MOUSE STANDARD; PRT; 716 AA.
AC P26928;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP).
GN Mst1 OR HGFL.
OS Mus musculus (Mouse).

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[illegible]

FT DISULFID 194 333 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 212 251 BY SIMILARITY.
 FT DISULFID 240 263 BY SIMILARITY.
 FT DISULFID 292 370 BY SIMILARITY.
 FT DISULFID 313 352 BY SIMILARITY.
 FT DISULFID 341 364 BY SIMILARITY.
 FT DISULFID 379 457 BY SIMILARITY.
 FT DISULFID 400 440 BY SIMILARITY.
 FT DISULFID 428 452 BY SIMILARITY.
 FT DISULFID 477 593 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 512 528 BY SIMILARITY.
 FT DISULFID 607 672 BY SIMILARITY.
 FT DISULFID 637 651 BY SIMILARITY.
 FT DISULFID 662 690 BY SIMILARITY.
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 19 19 P -> Q (IN GENOMIC SEQUENCE).
 SQ SEQUENCE 716 AA; 80588 MW; BBCE02EF85213AC6 CRC64;

Query Match 52.1%; Score 272.5; DB 1; Length 716;
 Best Local Similarity 55.4%; Pred. No. 9.6e-22;
 Matches 46; Conservative 11; Mismatches 25; Indels 1; Gaps 1;

QY 4 CHANGSGAGTSTVTGTCOSWSSMPHRTPEPNGLMNYCRNDADT-GP 62
 DB 379 CHGSGEQKRGVSQKTRKGVQCCWSESSTPHKQFPTSPAPQAGLANFCRNDGSDSGP 438
 QY 63 WCFTTDPISIRWEYCNLTSCDTE 85
 DB 439 WCYTLDPDLFDYCALQRCDDQ 461

RESULT 11
 HGF HUMAN STANDARD; PRT; 728 AA.
 AC 01-JUN-1990 (Rel. 13, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 GN (Hepatopoietin A).
 DE HGF OR HPTA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91340155; PubMed=1831432;
 RA Seki T., Hagiya M., Shimomishi M., Nakamura T., Shimizu S.;
 RT "Organization of the human hepatocyte growth factor-encoding gene.";
 RL Gene 102:213-219 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=89392017; PubMed=2528952;
 RA Miyazawa K., Teubouchi H., Naka D., Takahashi K., Okigaki M.,
 RA Arakaki N., Nakayama H., Hiroo S., Sakiyama O., Takahashi K.,
 RA Gohda E., Daikuhara Y., Kitamura N.;
 RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
 RT growth factor.";
 RL Biochem. Biophys. Res. Commun. 163:967-973 (1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=91025062; PubMed=2145836;
 RA Seki T., Ihara I., Sugimura A., Shimomishi M., Nishizawa T.,
 RA Asami O., Hagiya M., Nakamura T., Shimizu S.;
 RT "Isolation and expression of cDNA for different forms of hepatocyte
 RT growth factor from human leukocyte.";
 RL Biochem. Biophys. Res. Commun. 172:321-327 (1990).

RN [4]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 55-73 AND 495-520.
 RC TISSUE=Liver;
 RX MEDLINE=9006676; PubMed=2531289;
 RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimomishi M.,
 RA Sugimura A., Tashiro K., Shimizu S.;
 RT "Molecular cloning and expression of human hepatocyte growth factor.";
 RL Nature 342:440-443 (1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic fibroblast;
 RX MEDLINE=9134393; PubMed=1831266;
 RA Weidner K.M., Arakaki N., Hartmann G., Vandeckerckhove J., Weingart S.,
 RA Rieder H., Fontatsch C., Teubouchi H., Hishida T., Daikuhara Y.,
 RA Birnmeier W.;
 RT "Evidence for the identity of human scatter factor and human
 RT hepatocyte growth factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005 (1991).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Courtney L., Elliot G., Angell S.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 249-695 FROM N.A.
 RX MEDLINE=91369928; PubMed=1832556;
 RA Miyazawa K., Kitamura A., Kitamura N.;
 RT "Structural organization and the transcription initiation site of the
 RT human hepatocyte growth factor gene.";
 RL Biochemistry 30:9170-9176 (1991).
 RN [8]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=91207365; PubMed=1826837;
 RA Yoshiyama Y., Arakaki N., Naka D., Takahashi K., Hiroo S., Kondo J.,
 RA Nakayama H., Gohda E., Kitamura N., Teubouchi H., Ishii T.,
 RA Hishida T., Daikuhara Y.;
 RT "Identification of the N-terminal residue of the heavy chain of both
 RT native and recombinant human hepatocyte growth factor.";
 RL Biochem. Biophys. Res. Commun. 175:660-667 (1991).
 RN [9]
 RP CARBOHYDRATE-LINKAGE SITE THR-476.
 RX MEDLINE=93129192; PubMed=1482348;
 RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
 RA Nakamura T., Shimizu S.;
 RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
 RT on the alpha chain.";
 RL Biochem. Biophys. Res. Commun. 189:1329-1335 (1992).
 RN [10]
 RP MUTAGENESIS.
 RX MEDLINE=92331602; PubMed=1321034;
 RA Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
 RA Baker J.B., Godowski P.J.;
 RT "Structure-function analysis of hepatocyte growth factor:
 RT identification of variants that lack mitogenic activity yet retain
 RT high affinity receptor binding.";
 RL EMBO J. 11:2503-2510 (1992).
 RN [11]
 RP STRUCTURE BY NMR OF 31-127.
 RX MEDLINE=98154323; PubMed=9493272;
 RA Zhou H., Mazulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,
 RA Rubin J.S., Bottaro D.P., Byrd R.A.;
 RT "The solution structure of the N-terminal domain of hepatocyte growth
 RT factor reveals a potential heparin-binding site.";
 RL Structure 6:109-116 (1998).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.
 RX MEDLINE=99036858; PubMed=9817840;
 RA Ullrich M., Lokker N.A., Godowski P.J., de Vos A.M.;
 RT "Crystal structure of the NK1 fragment of human hepatocyte growth
 RT factor at 2.0-A resolution.";
 RL Structure 6:1383-1393 (1998).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 CC HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS
 CC AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.

IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 DISULFIDE BOND.
 -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 -1- SIMILARITY: Contains 4 kringle domains.
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 DR EMBL; D90334; BAA1348.1; -;
 DR EMBL; D90318; BAA1348.1; JOINED.
 DR EMBL; D90319; BAA1348.1; JOINED.
 DR EMBL; D90320; BAA1348.1; JOINED.
 DR EMBL; D90322; BAA1348.1; JOINED.
 DR EMBL; D90323; BAA1348.1; JOINED.
 DR EMBL; D90324; BAA1348.1; JOINED.
 DR EMBL; D90325; BAA1348.1; JOINED.
 DR EMBL; D90326; BAA1348.1; JOINED.
 DR EMBL; D90327; BAA1348.1; JOINED.
 DR EMBL; D90328; BAA1348.1; JOINED.
 DR EMBL; D90329; BAA1348.1; JOINED.
 DR EMBL; D90330; BAA1348.1; JOINED.
 DR EMBL; D90331; BAA1348.1; JOINED.
 DR EMBL; D90332; BAA1348.1; JOINED.
 DR EMBL; D90333; BAA1348.1; JOINED.
 DR EMBL; M29145; AAA52650.1; -;
 DR EMBL; M60718; AAA52648.1; -;
 DR EMBL; X16323; CAA34387.1; -;
 DR EMBL; M73239; AAA64239.1; -;
 DR EMBL; M73240; AAA64297.1; -;
 DR EMBL; AC004960; AAC71655.1; -;
 DR EMBL; M75983; AAG53460.1; -;
 DR EMBL; M75972; AAG53460.1; JOINED.
 DR EMBL; M75973; AAG53460.1; JOINED.
 DR EMBL; M75974; AAG53460.1; JOINED.
 DR EMBL; M75975; AAG53460.1; JOINED.
 DR EMBL; M75976; AAG53460.1; JOINED.
 DR EMBL; M75977; AAG53460.1; JOINED.
 DR EMBL; M75978; AAG53460.1; JOINED.
 DR EMBL; M75979; AAG53460.1; JOINED.
 DR EMBL; M75980; AAG53460.1; JOINED.
 DR EMBL; M75981; AAG53460.1; JOINED.
 DR EMBL; M75982; AAG53460.1; JOINED.
 DR PIR; JH0579; JH0579.
 DR PDB; 2HGJ; 24-JUN-98.
 DR PDB; 1BHT; 18-NOV-98.
 DR PDB; 1NK1; 29-DEC-99.
 DR MEROPS; S01.976; -;
 DR GlycoSiteDB; P14210; -;
 DR Gene; HGNC:4893; HGF.
 DR MIM; 142409; -;
 DR GO; GO:0008083; F: growth factor activity; NAS.
 DR InterPro; IPR001314; Cytocytin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0018; KRINGLE.
 DR ProDom; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN; AP; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.

DR PROSITE; PS00070; KRINGLE_2; 4.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 KW Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
 KM Signal; 3D-structure; Polymorphism; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 31
 FT CHAIN 32 454
 FT CHAIN 495 728
 FT MOD_RES 32 32
 FT DOMAIN 32 127
 FT DOMAIN 128 206
 FT DOMAIN 211 288
 FT DOMAIN 305 383
 FT DOMAIN 391 469
 FT DOMAIN 495 728
 FT DISULFID 70 96
 FT DISULFID 74 84
 FT DISULFID 128 206
 Query Match 51.4%; Score 269; DB 1; Length 728;
 Best Local Similarity 51.9%; Pred. No. 2.3e-21;
 Matches 42; Conservative 9; Mismatches 30; Indels 0; Gaps 0;
 QY 3 QCTHNGGQSYRGTFSTTVYGRGCGSSMTTPRHQRTPENYNDGLTMYCRNPADDTGP 62
 DB 210 ECWTCNGESYRGIMDTESGKTCQRPDHTQHPHKKFLPERYPDKGPDNYCRNPQGP 269
 QY 63 WCFTDPSIRMEYCNLTRCS 83
 DB 270 WCYTLDPHTRMEYCAIKTCAD 290
 RESULT 12
 ID HGF_MOUSE STANDARD; PRT; 728 AA.
 AC Q08648; O61662; O64007;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 DE (Hepatopoietin A).
 GN HGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOPFORMS LONG AND SHORT), AND SEQUENCE OF 496-504.
 RC TISSUE=Mammary fibroblast; PubMed=8135822;
 RX MEDLINE=94183257; PubMed=8135822;
 RA Sasaki M., Nishio M., Sasaki T., Enami J.,
 RT "Identification of mouse mammary fibroblast-derived mammary growth
 RT factor as hepatocyte growth factor.";
 RL Biochem. Biophys. Res. Commun. 199; 772-779 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94363381; PubMed=8081873;
 RA Lee C.C., Kozak C.A., Yamada K.M.;
 RT "Structure, genetic mapping, and expression of the mouse Hgf/scatter
 RT factor gene.";
 RL Cell Adhes. Commun. 1:101-111 (1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94060105; PubMed=8241272;
 RA Liu Y., Michalopoulos G.K., Zarnegar R.;
 RT "Molecular cloning and characterization of cDNA encoding mouse
 RT hepatocyte growth factor.";
 RL Biochim. Biophys. Acta 1216: 299-303 (1993).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 CC HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS AS
 CC GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES. IT
 CC HAS NO DETECTABLE PROTEASE ACTIVITY.

```

CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q08048-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q08048-2; Sequence=VSP_005408;
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 4 kringle domains.
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-----
CC EMBL: D10213; BAA01064.1; -
CC EMBL: D10213; BAA01065.1; -
CC EMBL: S71816; AAB31855.1; -
CC EMBL: X72307; CAA51054.1; ALT_INIT.
CC PIR: JC2117; A60185.
CC HSSP: P14210; 1BHT.
CC MEROPS: S01.982; -
CC MGD: MGI.96079; HGF.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR003014; PAN.
CC InterPro: IPR003609; Pan app.
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam: PF00051; Kringle; 4.
CC Pfam: PF00024; PAN; 1.
CC Pfam: PF00089; Lypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00018; KRINGLE.
CC ProDom: PD000395; Kringle; 4.
CC SMART: SM00130; KR; 4.
CC SMART: SM00473; PAN_Ap; 1.
CC SMART: SM00020; TRYD_Spc; 1.
CC SMART: PS00021; KRINGLE_1; 4.
CC PROSITE: PS00070; KRINGLE_2; 4.
CC PROSITE: PS0240; TRYPSIN_DOM; 1.
CC Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
CC Signal; Alternative splicing; Eyrilidone carboxylic acid.
CC SIGNAL: 1
CC CHAIN 33 495
CC CHAIN 496 728
CC MOD_RES 33 33
-----
CC DOMAIN 33 128
CC DOMAIN 129 207
CC DOMAIN 212 289
CC DOMAIN 306 384
CC DOMAIN 392 470
CC DOMAIN 496 728
CC DISULFID 71 97
CC DISULFID 75 85
CC DISULFID 488 607
CC CARBOHYD 295 295
CC CARBOHYD 403 403
CC CARBOHYD 463 463
CC CARBOHYD 569 569
CC CARBOHYD 656 656
CC VARSPLIC 163 167
-----
CC CONFLICT 344 344
CC CONFLICT 479 479
CC CONFLICT 564 564
CC SEQUENCE 728 AA; 82944 MM; A0381FC497534328 CRC64;
-----
Query Match 50.3%; Score 263; DB 1; Length 728;
Best Local Similarity 51.2%; Pred. No. 1e-20;

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Matches 41; Conservative 9; Mismatches 30; Indels 0; Gaps 0;
QY 3 OCYHNGSGS YRGSTFTVTRGTCQSSSWTTPRHORTENTENYNDLTINVCNPDADTGP 62
DB 211 ECMTGNSGSTRGPMHNTSGKTCRWDOCTPHRHFLEPRIPDKGFPDNYCNPDGKRRP 270
QY 63 WCFTTDPGSTRWEYCNITRCS 82
DB 271 WCYTLDPDPTWEYCAIKTCA 290
-----
RESULT 13
HGF RAT
ID HGF RAT STANDARD; PRT; 728 AA.
AC P17945;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoietin A).
GN HGF
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=90222197; PubMed=2139229;
RA Toshio K., Hagiya M., Nishizawa T., Seki T., Shimomichi M.,
RA Shimizu S., Nakamura T.;
RT "Deduced primary structure of rat hepatocyte growth factor and
RT expression of the mRNA in rat tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=91031482; PubMed=2146117;
RA Okajima A., Miyazawa K., Kitamura N.;
RT "Primary structure of rat hepatocyte growth factor and induction of
RT its mRNA during liver regeneration following hepatic injury.";
RL Eur. J. Biochem. 193:375-381(1990).
CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
CC HEPATOCYTE CELLS. SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS
CC AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 4 kringle domains.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
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CC EMBL: D90102; BAA14133.1; -
CC EMBL: X54400; CAA38266.1; -
CC PIR: A35644; A35644.
CC HSSP: P14210; 1BHT.
CC MEROPS: S01.978; -
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR003014; PAN.
CC InterPro: IPR003609; Pan app.
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam: PF00051; Kringle; 4.
CC Pfam: PF00024; PAN; 1.
CC Pfam: PF00089; Lypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.

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FT DISULFID 632 646 BY SIMILARITY.
FT DISULFID 657 685 BY SIMILARITY.
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 13 13 Y -> C.
FT VARIANT 212 212 /FTID=VAR_006631.
FT VARIANT 212 212 C -> F.
FT VARIANT 676 676 /FTID=VAR_006632.
FT VARIANT 676 676 E -> K (IN DBSNP:7798).
FT CONFLICT 623 623 /FTID=VAR_014569.
FT CONFLICT 623 623 L -> F (IN REF. 2).
SQ SEQUENCE 711 AA; 80379 MW; 596ED21F180290B4 CRC64;

Query Match 47.3%; Score 247.5; DB 1; Length 711;
Best Local Similarity 50.6%; Pred. No. 4.6e-19;
Matches 43; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

QY 2 ROCYHNGOSYRGTFSTVTGRTQSWSSMTPHRHQRTPEYVNDGLTMNYCRNPDADT-60
DB 368 QDCYHNGAGEYRGTVKTRKGVCCQMSATPHKPGFTFSEPHAGLEENFCNPDGDH 427
QY 61 GPCWCTTDPSSIRWEYCNLTRCSDE 85
DB 428 GPCWCTTDPPTPDYCALRRCADDO 452

RESULT 15
ID PLMN SHEEP STANDARD; PRT; 343 AA.
AC P81286;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN Plg.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=93149995; PubMed=1492092;
RA Schaller J., Straub C., Kamfer U., Rickli E.E.;
RT "Complete amino acid sequence of ovine miniplasminogen.";
RL Protein Seq. Data Anal. 5:21-25(1992).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAVIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains at least 2 kringle domains.
CC PIR; B61545; B61545.
CC HSSP; P00747; SHPG.
CC MEROPS; S01.233; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle_1.

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DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS50070; KRINGLE 2; 1.
DR PROSITE; PS50040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR HydroLase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
FT NON_TER 1 1
FT DOMAIN <1 140 HEAVY CHAIN A.
FT DOMAIN 141 >343 LIGHT CHAIN A.
FT DOMAIN <1 17 KRINGLE 4.
FT DOMAIN 41 120 KRINGLE 5.
FT ACT_SITE 114E 341 SERINE PROTEASE.
FT ACT_SITE 181 181 CHARGE RELAY SYSTEM.
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
FT ACT_SITE 319 319 CHARGE RELAY SYSTEM.
FT NON_TER 343 343
SQ SEQUENCE 343 AA; 37662 MW; 8DF6BBA92D596EEO CRC64;

Query Match 44.7%; Score 234; DB 1; Length 343;
Best Local Similarity 49.4%; Pred. No. 5.8e-18;
Matches 41; Conservative 12; Mismatches 28; Indels 2; Gaps 2;

QY 4 CYHNGOSYRGTFSTVTGRTQSWSSMTPHRHQRTPEYVNDGLTMNYCRNPDAD-TG 61
DB 15 CMLGIGKGYRGKATTTVAGVPGQEWAAQEPHRHGIFTETNPBAGLEKNYCRNPDGVNG 74
QY 62 PWCCTTDPSSIRWEYCNLTRCSDE 84
DB 75 PWCCTTNPRLKLPDYCDIPQCS 97

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Search completed: January 12, 2004, 17:23:57
 Job time : 7.69549 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:18:07 ; Search time 28.4398 Seconds
(without alignments)
807.553 Million cell updates/sec

Title: US-10-088-548-6
Perfect score: 523
Sequence: 1 VRCCHGNQSYRGFTSTV.....SIRWEXNLTIRCSDTEGTV 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriaph:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	98.9	113	4 Q9UR5	Q9UR5 homo sapien
2	485	92.7	454	6 O46506	O46506 papio hamad
3	444	84.9	810	4 Q15146	Q15146 homo sapien
4	439	83.9	132	4 Q16609	Q16609 homo sapien
5	433	79.0	113	4 Q9UR7	Q9UR7 homo sapien
6	408	78.0	105	4 Q9UR8	Q9UR8 homo sapien
7	405	77.4	113	4 Q9UR6	Q9UR6 homo sapien
8	404	77.2	359	6 Q8WNR1	Q8WNR1 canis fam11
9	400	76.5	812	11 Q91WJ5	Q91WJ5 mus musculu
10	395	75.5	145	6 Q28911	Q28911 macaca fasc
11	379.5	72.6	812	11 Q9R0W3	Q9R0W3 rattus norv
12	360	68.8	806	6 O18783	O18783 macropus eu
13	303	57.9	2869	6 Q28398	Q28398 erinaceus e
14	281	53.7	429	13 Q8AVB0	Q8AVB0 brachydanto
15	272.5	52.1	716	11 Q91XG8	Q91XG8 mus musculu
16	268.5	51.3	709	13 Q90ZM6	Q90ZM6 brachydanto

17	268.5	51.3	716	11 P70521	P70521 rattus norv
18	264	50.5	728	11 Q8C95	Q8C95 mus musculu
19	262	50.1	285	4 Q8CE2	Q8CE2 homo sapien
20	262	50.1	290	4 Q02935	Q02935 homo sapien
21	258	49.3	296	4 Q14519	Q14519 homo sapien
22	257.5	49.2	385	5 Q25101	Q25101 herdamia m
23	256.5	49.0	716	13 Q91691	Q91691 xenopus lae
24	256.5	49.0	728	6 Q9BH09	Q9BH09 felis silve
25	255.5	48.9	947	13 Q8AXY6	Q8AXY6 gallus gall
26	254	48.6	334	6 Q46507	Q46507 papio hamad
27	249.5	47.7	209	11 Q8BS17	Q8BS17 mus musculu
28	247.5	47.3	208	4 Q9BYM0	Q9BYM0 homo sapien
29	247.5	47.3	210	4 Q13494	Q13494 homo sapien
30	246.5	47.1	109	6 Q9N1B8	Q9N1B8 ovis aries
31	246.5	47.1	710	13 Q91402	Q91402 xenopus. he
32	246.5	47.1	717	13 P70006	P70006 xenopus lae
33	243.5	46.6	313	13 Q9PU78	Q9PU78 crocodylus
34	243.5	46.6	567	4 Q13208	Q13208 homo sapien
35	243.5	46.6	948	5 Q9Y1Y6	Q9Y1Y6 ephydactia f
36	242	46.3	726	13 Q90978	Q90978 gallus gall
37	241.5	46.2	211	11 Q55027	Q55027 mus musculu
38	241.5	46.2	215	13 Q42341	Q42341 gallus gall
39	239.5	45.8	704	13 Q90865	Q90865 gallus gall
40	237.5	45.4	946	13 Q07153	Q07153 torpedo cal
41	232.5	44.5	648	4 Q9H1V4	Q9H1V4 homo sapien
42	223	42.6	53	4 Q9UM12	Q9UM12 homo sapien
43	220.5	42.6	95	4 Q8V696	Q8V696 homo sapien
44	220.5	42.2	930	13 Q8AV69	Q8AV69 xenopus lae
45	212.5	40.6	801	11 Q8K0Q8	Q8K0Q8 mus musculu

ALIGNMENTS

RESULT 1
ID Q9UR5 PRELIMINARY; PRT; 113 AA.
AC Q9UR5;
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Apolipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2181705; PubMed=11285247;
RA Ogorzelkova M., Kraft H.G., Ehnholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158663; AA03680.1; JOINED.
DR EMBL; AF158662; AA03680.1; JOINED.
DR HSP; P00747; IPMK.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR GlycoProtein; Kringle; Lipoprotein.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12685 MM; F3D65681D9B5253A CRC64;
Query Match 98.9%; Score 517; DB 4; Length 113;
Best Local Similarity 98.9%; Pred. No. 1.7e-52;

Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRQCYHNGOSYRGFTSTVTGRTCSQSSMTPHRHQRTPEPNYPNDGLTMNYCRNPADT 60
 DB 8 VRQCYHNGOSYRGFTSTVTGRTCSQSSMTPHRHQRTPEPNYPNDGLTMNYCRNPADT 67

QY 61 GPWCFTTDPISIRWEYCNLTRCSDTGTVV 89
 DB 68 GPWCFTTDPISIRWEYCNLTRCSDTGTVV 96

RESULT 2
 046506 PRELIMINARY; PRT; 454 AA.

AC 046506; PRELIMINARY; PRT; 454 AA.
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Apolipoprotein a (Fragment).
 GN BABAOA.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OC NCBI_TaxId=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cox L.A., Jett C., Hixson J.E.;
 RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
 RT Site Mutation is Associated with Deletion of a Single Exon in a Null
 RT Allele."
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 51.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC EMBL: AF029691; AAB97886.1; -.
 DR HSSP: P00747; 2PK4.
 DR MEROPS: S01.999; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00051; kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00019; KRINGLE.
 DR ProDom: PD000395; Kringle; 2.
 DR SMART: SM00130; KR; 2.
 DR SMART: SM00020; TRY. Spc; 1.
 DR PROSITE: PS00021; KRINGLE_1; 2.
 DR PROSITE: PS50070; KRINGLE_2; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Glycoprotein; Hydrolyase; Kringle; Lipoprotein; Protease;
 KW Serine protease.
 FT NON TER
 FT SEQUENCE 1 1
 SQ SEQUENCE 454 AA; 50041 MW; 974E30744C187B2F CRC64;

Query Match 92.7%; Score 485; DB 6; Length 454;
 Best Local Similarity 89.9%; Pred. No. 4.2e-46;
 Matches 80; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 VRQCYHNGOSYRGFTSTVTGRTCSQSSMTPHRHQRTPEPNYPNDGLTMNYCRNPADT 60
 DB 99 VRQCYHNGOSYRGFTSTVTGRTCSQSSMTPHRHQRTPEPNYPNDGLTMNYCRNPADT 158

QY 61 GPWCFTTDPISIRWEYCNLTRCSDTGTVV 89
 DB 159 GPWCFTTDPISIRWEYCNLTRCSDTGTVV 187

RESULT 3
 015146 PRELIMINARY; PRT; 810 AA.
 AC 015146; PRELIMINARY; PRT; 810 AA.

DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Plasminogen precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Liver;
 RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
 RA Mitchell D., Robinson J.H.;
 RT "Expression of recombinant human plasminogen and aglycoplasminogen in
 RT HeLa cells."
 RL Fibrinolysis 0.0-0.0 (1991).
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC EMBL: M74220; AAA6451.1; -.
 DR HSSP: P00747; 2PK4.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00051; kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 5.
 DR SMART: SM00130; KR; 5.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRY. Spc; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS50070; KRINGLE_2; 5.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Hydrolyase; Kringle; Protease; Serine protease; Signal.
 FT SIGNAL
 FT CHAIN 1 19 POTENTIAL.
 FT 20 810 PLASINOGEN.
 SQ SEQUENCE 810 AA; 90555 MW; B05C7D4BD0D20B3C CRC64;

Query Match 84.9%; Score 444; DB 4; Length 810;
 Best Local Similarity 82.0%; Pred. No. 4.7e-43;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGOSYRGFTSTVTGRTCSQSSMTPHRHQRTPEPNYPNDGLTMNYCRNPADT 60
 DB 374 VRQCYHNGOSYRGFTSTVTGRTCSQSSMTPHRHQRTPEPNYPNDGLTMNYCRNPADT 433

QY 61 GPWCFTTDPISIRWEYCNLTRCSDTGTVV 89
 DB 434 GPWCFTTDPISIRWEYCNLTRCSDTGTVV 462

RESULT 4
 016609 PRELIMINARY; PRT; 132 AA.
 ID 016609; PRELIMINARY; PRT; 132 AA.
 AC 016609; PRELIMINARY; PRT; 132 AA.
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE (APOARGC).
 GN APOARGC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Liver;
 RX MEDLINE=95268939; PubMed=7749817;
 RA Byrne C.D., Schwartz K., Lawn R.M.;
 RT "Loss of a splice donor site at a 'skipped exon' in a gene homologous
 to apolipoprotein(a) leads to an mRNA encoding a protein consisting of
 a single kringle domain."
 RL Arterioscler. Thromb. Vasc. Biol. 15:65-70(1995).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL: U9518; AA85693.1; -;
 DR EMBL: U9517; AA85692.1; -;
 DR HSSP: P00747; 1PMK.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; kringle; 1.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 KW Glycoprotein; Kringle.
 SQ SEQUENCE 132 AA; 14866 MW; 3794AD30A586DBA CRC64;

Query Match 83.3%; Score 439; DB 4; Length 132;
 Best Local Similarity 79.5%; Pred. No. 2.4e-43;
 Matches 70; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 VRCYCHNGSGSYRGFTSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDDT 60
 DB 25 VDCYCHNGSGSYRGFTSTVTGRTCSWSSMTPHQSRTPDEKYPNDGLTMNYCRNPDCSA 84
 QY 61 GPWCFTTDPISIRMEYCNLTRCSDTGTV 88
 DB 85 GPWCYTTDPNVMEYCNLTRCSDEGTV 112

RESULT 5

ID Q9UR7 PRELIMINARY; PRT; 113 AA.
 AC Q9UR7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).
 GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21181705; PubMed=11285247;
 RA Ogorelkova M., Kraft H.G., Rhinholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
 RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
 RT different patterns in Africans and Caucasians."
 RL Hum. Mol. Genet. 10:815-824(2001).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL: AF158659; AAF03678.1; -;
 DR EMBL: AF158658; AAF03678.1; JOINED.
 DR HSSP: P00747; 2PK4.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; kringle; 1.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 KW Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 113 AA; 12815 MW; 4F80AD8708548CB CRC64;

Query Match 79.0%; Score 413; DB 4; Length 113;
 Best Local Similarity 77.5%; Pred. No. 2.1e-40;

Matches 69; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 VRCYCHNGSGSYRGFTSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDDT 60
 DB 8 VDCYCHNGSGSYRGFTSTVTGRTCSWSSMTPHHQRTEYYPNDGLTMNYCRNPDAEI 67
 QY 61 GPWCFTTDPISIRMEYCNLTRCSDTGTV 89
 DB 68 GPWCYTTDPNVMEYCNLTRCSDEGTV 96

RESULT 6

ID Q9UR8 PRELIMINARY; PRT; 105 AA.
 AC Q9UR8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).
 GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21181705; PubMed=11285247;
 RA Ogorelkova M., Kraft H.G., Rhinholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
 RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
 RT different patterns in Africans and Caucasians."
 RL Hum. Mol. Genet. 10:815-824(2001).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL: AF158656; AAF03677.1; -;
 DR EMBL: AF158655; AAF03677.1; JOINED.
 DR HSSP: P00747; 2PK4.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; kringle; 1.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 KW Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 105 AA; 11882 MW; 6ECB6C02CD30EFA2 CRC64;

Query Match 78.0%; Score 408; DB 4; Length 105;
 Best Local Similarity 75.3%; Pred. No. 7.4e-40;
 Matches 67; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 VRCYCHNGSGSYRGFTSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDDT 60
 DB 8 VDCYCHNGSGSYRGFTSTVTGRTCSWSSMTPHHQRTEYYPNDGLTMNYCRNPDAEI 67
 QY 61 GPWCFTTDPISIRMEYCNLTRCSDTGTV 89
 DB 68 GPWCYTTDPNVMEYCNLTRCSDEGTV 96

RESULT 7

ID Q9UR6 PRELIMINARY; PRT; 113 AA.
 AC Q9UR6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).
 GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2181705; PubMed=11285247;
 RA Ogorekova M., Kraft H.G., Enholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
 RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
 RT different patterns in Africans and Caucasians."
 RL Hum. Mol. Genet. 10:815-824(2001).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; AF158661; AF03679.1; -
 DR EMBL; AF158660; AF03679.1; JOINED.
 DR HSSP; P00747; 2PK4.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 KM Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 FT 113 113
 SQ SEQUENCE 113 AA; 12697 MW; 51D4461D9C6312E CRC64;
 Query Match 77.4%; Score 405; DB 4; Length 113;
 Best Local Similarity 75.3%; Pred. No. 1.8e-39;
 Matches 67; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
 OY 1 VROCYHNGOSYRGSTSTVTGRTCSWSMTPRHQRTPENYPNGLTMNYCRNPADAT 60
 DB 8 VQCYHGDGSGYSGISTTITGRTCSWSMTPRHQRTPENYPNGLTMNYCRNPADGK 67
 OY 61 GPMCFITDPSIRMEYCNLTGCSDEGTIV 89
 DB 68 QPMCYTTPCVRWEYCNLTGCSDETSGLV 96
 Db
 RESULT 8
 O8WMR1 PRELIMINARY; PRT; 359 AA.
 AC O8WMR1;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Plasmidogen (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxId=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pyle-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kiaker O.,
 RA Folkman J., Waters D.J.;
 RT "Angiotensin is detectable in the urine of dogs with spontaneous Bone
 RT Cancer".
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 DR EMBL; AY069985; AAL58519.1; -
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003966; Prothrombin.
 DR Pfam; PF00051; Kringle; 4.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 4.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS00070; KRINGLE_2; 4.
 KM Glycoprotein; Kringle.
 FT NON_TER 1
 FT 359 359
 SQ SEQUENCE 359 AA; 41172 MW; 776D35FAAB0BD9E CRC64;

Query Match 77.2%; Score 404; DB 6; Length 359;
 Best Local Similarity 77.8%; Pred. No. 8.5e-39;
 Matches 63; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
 OY 1 VROCYHNGOSYRGSTSTVTGRTCSWSMTPRHQRTPENYPNGLTMNYCRNPADAT 60
 DB 279 VQCYHNGOSYRGSTSTITGRTCSWSMTPRHQRTPENYPNGLTMNYCRNPADGK 338
 OY 61 GPMCFITDPSIRMEYCNLTGCS 81
 DB 339 SPWCYTTPSVRMEFCNLRKC 359
 Db

RESULT 9
 O91WJ5 PRELIMINARY; PRT; 812 AA.
 AC O91WJ5;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Plasmidogen.
 GN Plg.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Liver;
 RA Strassberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv.
 RA Bratwalte M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
 RA Nagaraja R.;
 RT "Genomic Sequence Analysis in the Mouse t-complex Region."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 DR EMBL; BC014773; AA14773.1; -
 DR EMBL; AF481053; AA22156.1; -
 DR HSSP; P00761; 1AN1.
 DR MGD; MGI:97620; Plg.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR InterPro; IPR001400; Somatotropin.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;
 Query Match 76.5%; Score 400; DB 11; Length 812;
 Best Local Similarity 70.8%; Pred. No. 6.2e-38;
 Matches 63; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
 OY 1 VROCYHNGOSYRGSTSTVTGRTCSWSMTPRHQRTPENYPNGLTMNYCRNPADAT 60
 DB 374 VQCYHGDGSGYSGISTTITGRTCSWSMTPRHQRTPENYPNGLTMNYCRNPADGK 433

QY 61 GPMCFITDPSIRMEYCNLTRCSDTEGTV 89
 DB 434 GPMCFITDPSIRMEYCNLTRCSDTEGTV 462

RESULT 10

Q28911 PRELIMINARY; PRT; 145 AA.
 ID 028911
 AC 028911;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).
 GN APOLIPOPROTEIN(A).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9541;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95395387; PubMed=7666007;
 RA Ramnarack R., Spanh M.A., Hicks G.W., Kieft K.A., Brammer D.W.,
 RA Minton L.L.; Newton R.S.;
 RT "Gemfibrozil significantly lowers cynomolgus monkey plasma
 RT lipoprotein(a)-protein and liver apolipoprotein(a) mRNA levels";
 RL J. Lipid Res. 36:1294-1304(1995).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; S79621; AAD14312.1; -.
 DR HSSP; P00747; 2PKA.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR GlycoProtein; Kringle; Lipoprotein.
 FT NON TER 145
 SQ SEQUENCE 145 AA; 16097 MW; 0D2DA20A06A5D87 CRC64;
 Query Match 75.5%; Score 395; DB 6; Length 145;
 Best Local Similarity 73.0%; Pred. No. 3.4e-38;
 Matches 65; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 1 VROCHNGSGYRGFTSTVTGRTQSGSSMTPHRQRTPEPNYRNDGLTMYCRNPDADT 60
 DB 40 VDDCYGHDQSYOGTSTVTGRTQAGSMSEPHQNRRTENYRNDGLTMYCRNPDPA 99
 QY 61 GPMCFITDPSIRMEYCNLTRCSDTEGTV 89
 DB 100 APICYTMDPVRMEYCNLTRCSDAEGTAV 128
 RESULT 11
 Q28903 PRELIMINARY; PRT; 812 AA.
 ID 028903;
 AC 028903;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Plasminogen protein precursor (EC 3.4.21.7).
 GN PLASMINOGEN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Bangert K., Johnsen A.H., Thorsen S.;
 RT "Rat plasminogen: cDNA and gene structure";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91250378; PubMed=1645711;
 RA Kanalas J.U., Makker S.P.;
 RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
 RT receptor site for plasminogen.";
 RL J. Biol. Chem. 266:10825-10829(1991).
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 DR EMBL; AJ242649; CAB46014.1; -.
 DR HSSP; P00747; 1PMK.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR001400; Somatostatin.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00130; KR; 4.
 DR PROSITE; PS00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00338; SOMATOSTATIN_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR GlycoProtein; Hydrolyase; Kringle; Protease; Serine protease; Signal.
 FT SIGNAL 1
 FT CHAIN 20 812 PLASMINOGEN.
 SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410B9C9E CRC64;

Query Match 72.6%; Score 379.5; DB 11; Length 812;
 Best Local Similarity 71.9%; Pred. No. 1.5e-35;
 Matches 64; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
 QY 1 VROCHNGSGYRGFTSTVTGRTQSGSSMTPHRQRTPEPNYRNDGLTMYCRNPDADT 59
 DB 373 VOECYQNGKSYRGFTSTVTGRTQSGSSMTPHRQRTPEPNYRNDGLTMYCRNPDADT 432
 QY 60 TGPWCFTDPSIRMEYCNLTRCSDTEGTV 88
 DB 433 RGPWCFTDPSIRMEYCNLTRCSDTEGTV 461
 RESULT 12
 Q18783 PRELIMINARY; PRT; 806 AA.
 ID 018783;
 AC 018783;
 DT 01-JAN-1998 (T-EMBLrel. 05, Created)
 DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Plasminogen.
 GN Plasminogen.
 OS Macropus eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 NCBI_TaxID=9315;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98004511; PubMed=9342350;
 RA Lam R.M., Schwartz K., Patchy L.;
 RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 DR EMBL; AF012297; AAB65760.1; -.

DR HSSP; P00747; SHPG.
 DR MEROPS; S01.233; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser protease_Try.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00051; PAN; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR GlycoProtein; Hydrolyase; Kringle; Protease; Serine protease.
 KW GlycoProtein; Hydrolyase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;

Query Match 68.8%; Score 360; DB 6; Length 806;
 Best Local Similarity 59.6%; Pred. No. 2.7e-33; Indels 0; Gaps 0;
 Matches 53; Conservative 20; Mismatches 16;

Qy 1 VROCYNHGSGSYRGTFSTVTGRTQGSWSMTPHRHQRTPENYNDGLTMNYCRNPADT 60
 Db 368 IQCEYBEGKNYGTSTTISGKKQCMSSMTPHQHKTDNPNMDLINYCRNPDGDK 427
 Qy 61 GPWCFTTDPBSIRMEYCNLTCSDEGTIV 89
 Db 428 SPWCYTMDPTVRWEFCNLKCGSTGL 456

RESULT 13
 Q28398 PRELIMINARY; PRT; 2869 AA.
 ID Q28398
 AC Q28398;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
 NCBI_TaxID=9365;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96025778; PubMed=7592597;
 RA Lavin R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
 BA Byrne C.D., Pong K.J., Meer K., Patchy L.;
 RT "The recurring evolution of lipoprotein(a). Insights from cloning of
 RT hedgehog apolipoprotein(a).";
 RL J. Biol. Chem. 270:24004-24009(1995).
 CC -1- SIMILARITY: CONTAINS 31 KRINGLE DOMAINS.
 DR EMBL; U01170; AAC48522.1; -
 DR HSSP; P00747; SHPG.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 31.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 31.
 DR SMART; SM00130; KR; 31.
 DR PROSITE; PS00021; KRINGLE_1; 30.
 DR PROSITE; PS00070; KRINGLE_2; 31.
 KW GlycoProtein; Kringle; Lipoprotein.
 FT NON TER 1
 SQ SEQUENCE 2869 AA; 318601 MW; 9527CEP985A4FB2A CRC64;

Query Match 57.9%; Score 303; DB 6; Length 2869;
 Best Local Similarity 58.2%; Pred. No. 4.8e-26;
 Matches 46; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Qy 3 OCHYHNGSGSYRGTFSTVTGRTQGSWSMTPHRHQRTPENYNDGLTMNYCRNPADT 62
 Db 2776 OCLKNGSGSYRGTSVGTGRTQGSWSMTPHRHQRTPENYNDGLTMNYCRNPADT 2835
 Qy 63 WCFTTDPBSIRMEYCNLTCSDEGTIV 81
 Db 2836 WCFTTDPBSIRMEYCNLTCSDEGTIV 2854

RESULT 14
 ID Q8A8B0 PRELIMINARY; PRT; 429 AA.
 AC Q8A8B0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Plasminogen precursor (Fragment).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hanumanthiah R., Day K., Jagadeeswaran P.;
 RT "Comprehensive analysis of blood coagulation pathways in teleostei:
 RT Evolution of coagulation factor genes and identification of zebrafish
 RT factor VIIa.";
 RL Blood Cells Mol. Dis. 0:0-0(2002).
 DR EMBL; AF515276; AAN71006.1; -
 FT NON TER 1
 SQ SEQUENCE 429 AA; 47556 MW; 9A580A21A549C12 CRC64;

Query Match 53.7%; Score 281; DB 13; Length 429;
 Best Local Similarity 57.3%; Pred. No. 2.1e-24;
 Matches 47; Conservative 12; Mismatches 21; Indels 2; Gaps 2;

Qy 2 RCHYHNGSGSYRGTFSTVTGRTQGSWSMTPHRHQRTPENYNDGLTMNYCRNPADT 59
 Db 100 KCKKNGSGSYRGTSVGTGRTQGSWSMTPHRHQRTPENYNDGLTMNYCRNPADT 159
 Qy 60 TGPWCFTTDPBSIRMEYCNLTCSDEGTIV 81
 Db 160 NGPWCYTMDPTVRWEFCNLKCGSTGL 181

RESULT 15
 ID Q91XG8 PRELIMINARY; PRT; 716 AA.
 AC Q91XG8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hepatocyte growth factor-like.
 GN HGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 DR EMBL; BC010551; AAH10551.1; -
 DR HSSP; P00761; IAN1.
 DR MGD; MGI:96080; Hgfl.

DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003019; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR003366; Prothombin.
DR InterPro: IPR001254; Ser_protase_Try.
DR Pfam: PF00051; kringle; 4.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHOMBIN.
DR PRINTS: PD000395; Kringle; 4.
DR ProDom: PD00130; KR; 4.
DR SMART: SM00130; KR; 4.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00021; KRINGLE_1; 4.
DR PROSITE: PS00070; KRINGLE_2; 4.
DR PROSITE: PS02040; TRYPSIN_DOM; 1.
KW Glycoprotein. Hydrolase. Kringle. Protease. Serine protease.
SQ SEQUENCE 716 AA; 80693 MW; 12474C48A7D9B46D CRC64;

Query Match	52.1%	Score	272.5	DB	11	Length	716
Best Local Similarity	55.4%	Pred	No	3.6e-23			
Matches	46	Conservative	11	Mismatches	25	Indels	1
						Gaps	1

QY	Db	QY	Db
4	379	63	439
CYHANGGSGYGTGTTTGTGTCOSMSMPPHHORTPEMYPDGLTMMYCNENPADT-GP	CYHSGSGQYNGSVSKTRKGVQCCHMSSETPPHKPGTPTPSAPQAGLEAFNCNPPGDSDHP	MCFTTDPSTIMEYCNLTRCSDE	MCYTLDPDLTFDYCALQRCDDQ
62	438	85	461

Search completed: January 12, 2004, 17:25:37
Job time : 28.4398 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:16:07 ; Search time 35.4662 Seconds
(without alignments)
398.314 Million cell updates/sec

Title: US-10-088-548-6
Perfect score: 523
Sequence: 1 VRQCHGNQSYRGFTSTV.....SIRWEXNLTROCDPTEGTV 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_190un03.*
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523	100.0	89	22	AAV72946
2	523	100.0	308	22	AAV72944
3	444	84.9	90	21	AAAB01909
4	444	84.9	189	21	AAAB01918
5	444	84.9	192	21	AAAB01919
6	444	84.9	364	21	AAAB01905
7	444	84.9	369	21	AAV53868
8	444	84.9	374	21	AAV79226
9	444	84.9	375	21	AAV79225

10	444	84.9	378	17	AAW07579
11	444	84.9	378	21	AAAB1650
12	444	84.9	378	21	AAAB4894
13	444	84.9	380	20	AAV02105
14	444	84.9	437	19	AAW51457
15	444	84.9	452	21	AAV79224
16	444	84.9	453	20	AAW95051
17	444	84.9	458	23	ABW75941
18	444	84.9	467	13	AAW22499
19	444	84.9	476	13	AAW22503
20	444	84.9	484	24	AAW79749
21	444	84.9	563	23	ABW75942
22	444	84.9	566	20	AAV02100
23	444	84.9	571	23	ABW75944
24	444	84.9	576	23	ABW75943
25	444	84.9	790	15	AAW60519
26	444	84.9	790	22	AAW36562
27	444	84.9	791	18	AAW34285
28	444	84.9	791	21	AAW01887
29	444	84.9	791	21	AAV99589
30	444	84.9	791	21	AAV50867
31	444	84.9	791	22	AAW67223
32	444	84.9	791	23	AAW23660
33	444	84.9	791	23	ABW76087
34	444	84.9	807	13	AAW20013
35	444	84.9	810	11	AAW08065
36	444	84.9	810	12	AAW13219
37	444	84.9	810	12	AAW12406
38	444	84.9	810	12	AAW13220
39	444	84.9	810	12	AAW13221
40	444	84.9	810	12	AAW12938
41	444	84.9	810	14	AAW34428
42	444	84.9	810	18	AAW31169
43	444	84.9	810	20	AAV06885
44	444	84.9	810	20	AAV02114
45	444	84.9	810	21	AAW82690

ALIGNMENTS

RESULT 1
ID AAV72946
AAV72946 standard; Protein; 89 AA.
XX
AC AAV72946;
XX
XX
DT 13-JUN-2001 (first entry)
XX
DE Human apolipoprotein(a) kringle domain IV37, LK7 protein.
XX
XX Human; angiogenesis inhibitor; LK7; apolipoprotein(a) kringle domain;
KW angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy;
KW cytostatic; antineoplastic; antiarthritic; antipsoriatic; psoriasis;
KW ocular angiogenic disease; endothelial cell proliferation; tumour;
KW cell migration.
XX
XX Homo sapiens.
OS
XX
XX WO200119868-A1.
PN
XX
PD 22-MAR-2001.
XX
PF 15-SEP-1999; 99WO-KR00554.
XX
PR 15-SEP-1999; 99WO-KR00554.
XX
PA (MOGA-) MOGAM BIOTECHNOLOGY RRS INST.
XX
XX Chang J, Kim JS, Park EJ, Yum J, Chung S;
PI
XX WPI; 2001-244787/25.
DR
XX N-PSDB; AAD03257.

XX Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
PT diseases, e.g. cancer and rheumatoid arthritis, has human
PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT sequence -
PS Claim 2; Page 45-46; 50pp; English.

XX The present sequence is human LK7 protein which contains the amino
CC acid sequence of human apolipoprotein(a) kringle domain IV37
CC (KIV37). The human apolipoprotein(a) kringle domains IV36 (LK6
CC protein), IV37 (LK7 protein) and V38 (LK8 protein) together form the
CC angiogenesis inhibitor, LK68 protein. LK68, LK6, LK7 and LK8 are
CC inhibitors are of endothelial cell proliferation, cell migration and
CC normal development of capillaries in the chick embryo chorioallantoic
CC membrane (CAM). LK68 protein, its single kringle or their functional
CC equivalents, are useful for treating angiogenesis-mediated diseases,
CC such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
CC disease in animals or humans. LK68 is useful as an anticancer agent and
CC also for inhibiting primary tumour growth.

XX Sequence 89 AA;
SQ

Query Match 100.0%; Score 523; DB 22; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.2e-46;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRQCHNGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENPNGLTMNYCRNPDAOT 60
DB 1 VRQCHNGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENPNGLTMNYCRNPDAOT 60
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTIV 89
DB 61 GPMCFITDPSIRWEYCNLTRCSDTEGTIV 89

RESULT 2
AA72944
AA72944 standard; Protein; 308 AA.

AC AA72944;
DT 13-JUN-2001 (first entry)

XX Human angiogenesis inhibitor, LK68 protein.
DE Human angiogenesis inhibitor, LK68 protein.
XX
XX Human; angiogenesis inhibitor; LK68; apolipoprotein(a) kringle domain;
XX angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy;
XX cytostatic; antirheumatic; antiarthritic; antiproliferative; prostatic;
XX ocular angiogenic disease; endothelial cell proliferation; tumour;
XX cell migration.
XX
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
FH 1..91
FT /label= KIV36
FT /note= "Apolipoprotein(a) kringle domain IV36, LK6
FT protein"
FT /label= KIV37
FT /note= "Apolipoprotein(a) kringle domain IV37, LK7
FT protein"
FT /label= KIV38
FT /note= "Apolipoprotein(a) kringle domain V38, LK8
FT protein"
XX
XX WO200119868-A1.
XX
XX 22-MAR-2001.
XX
XX 15-SEP-1999; 99WO-KR00554.

XX 15-SEP-1999; 99WO-KR00554.
PR
XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
PA
XX Chang J, Kim JS, Park EJ, Yum J, Chung S;
PI
XX WPI; 2001-24787/25.
DR
XX N-PSDB; AAD03255.
DR
XX
XX Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
PT diseases, e.g. cancer and rheumatoid arthritis, has human
PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT sequence -
PS Claim 4; Page 42-44; 50pp; English.

XX The present sequence is human angiogenesis inhibitor, LK68 protein.
CC LK68 protein contains the amino acid sequences of human apolipoprotein(a)
CC kringle domains IV36 (LK6 protein), IV37 (LK7 protein) and V38
CC (LK8 protein). LK68, LK6, LK7 and LK8 are inhibitors are of endothelial
CC cell proliferation, cell migration and normal development of capillaries
CC in the chick embryo chorioallantoic membrane (CAM). LK68 protein, its
CC single kringle or their functional equivalents, are useful for
CC treating angiogenesis-mediated diseases, such as cancer, rheumatoid
CC arthritis, psoriasis or ocular angiogenic disease in animals or humans.
CC LK68 is useful as an anticancer agent and also for inhibiting primary
CC tumour growth.

XX Sequence 308 AA;
SQ

Query Match 100.0%; Score 523; DB 22; Length 308;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRQCHNGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENPNGLTMNYCRNPDAOT 60
DB 119 VRQCHNGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENPNGLTMNYCRNPDAOT 178
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTIV 89
DB 179 GPMCFITDPSIRWEYCNLTRCSDTEGTIV 207

RESULT 3
AAB01909
ID AAB01909 standard; Protein; 90 AA.

AC AAB01909;
DT 18-SEP-2000 (first entry)

XX Human plasminogen kringle 4 (Val354-Val443).
DE Human plasminogen kringle 4 (Val354-Val443).
XX
XX Plasminogen; human; kringle domain; endothelial cell proliferation;
XX angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
XX antiproliferative; antirheumatic; antitumor; antiproliferative;
XX antiproliferative; cancer; tumour; autoimmune disease.
XX
XX Homo sapiens.
OS
XX
XX US6057122-A.
XX
XX 02-MAY-2000.
XX
XX 05-MAY-1997; 97US-0851350.
XX
XX 03-MAY-1996; 96US-0643219.
XX 03-APR-1997; 97US-0832087.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Davidson DJ;
XX

XX WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
XX disorders such as angiogenic, ocular, skin diseases and cancer,
XX involves mixing mammalian plasminogen and elastase followed by
XX incubation and isolation -

XX Example 17; Page -: 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5
XX peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating
XX the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
XX endothelial cell proliferation and migration. The peptides are useful
XX for treating angiogenic diseases, primary and metastatic solid tumours
XX and carcinomas of various organs such as breast, genital tract,
XX endocrine glands, skin, tumours of the brain and eyes and solid tumours
XX arising from haematopoietic malignancies such as leukaemias and
XX lymphomas. They are also used for the prophylaxis of various autoimmune
XX diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
XX (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
XX Syndrome), diseases caused by excessive or abnormal stimulation of
XX endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
XX which have angiogenesis as a pathologic consequence (e.g., cat scratch
XX disease and ulcers). The peptides are also useful as a birth control
XX agent which inhibits ovulation and establishment of the placenta.
XX Sequences AAB01906-B01919 represent fragments of human plasminogen used
XX in an exemplification of the invention.
XX Note: This sequence is not shown in the specification, but is derived
XX from the full length human plasminogen sequence (AAB01887) shown in
XX figure 1.

XX Sequence 90 AA;

Query Match 84.9%; Score 444; DB 21; Length 90;
Best Local Similarity 82.0%; Pred. No. 6.2e-38;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VROCHNGGSGYRGFTSTVTGRTQSSWMTPHRHQRTPEPNYDGLTMNYCRNPDADT 60
DB 2 VDCYHGDGQSYRGFTSTVTGRTQSSWMTPHRHQRTPEPNYDGLTMNYCRNPDADK 61

QY 61 GPWCFTTDPISIRWEXCNLTRCSDTEGTV 89
DB 62 GPWCFTTDPISIRWEXCNLTRCSDTEASV 90

RESULT 4

AAB01918 standard; Protein; 189 AA.

AC AAB01918;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringles 4-5 (Val355-Ala543).

XX Plasminogen; human; kringle domain; endothelial cell proliferation;
XX angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
XX antipsoiatric; antiinflammatory; anticancer; antirheumatic; antiarthritic;
XX antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

XX Davidson DJ;

XX WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
XX disorders such as angiogenic, ocular, skin diseases and cancer,
XX involves mixing mammalian plasminogen and elastase followed by
XX incubation and isolation -

XX Example 17; Page -: 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5
XX peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating
XX the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
XX endothelial cell proliferation and migration. The peptides are useful
XX for treating angiogenic diseases, primary and metastatic solid tumours
XX and carcinomas of various organs such as breast, genital tract,
XX endocrine glands, skin, tumours of the brain and eyes and solid tumours
XX arising from haematopoietic malignancies such as leukaemias and
XX lymphomas. They are also used for the prophylaxis of various autoimmune
XX diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
XX (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
XX Syndrome), diseases caused by excessive or abnormal stimulation of
XX endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
XX which have angiogenesis as a pathologic consequence (e.g., cat scratch
XX disease and ulcers). The peptides are also useful as a birth control
XX agent which inhibits ovulation and establishment of the placenta.
XX Sequences AAB01906-B01919 represent fragments of human plasminogen used
XX in an exemplification of the invention.
XX Note: This sequence is not shown in the specification, but is derived
XX from the full length human plasminogen sequence (AAB01887) shown in
XX figure 1.

XX Sequence 189 AA;

Query Match 84.9%; Score 444; DB 21; Length 189;
Best Local Similarity 82.0%; Pred. No. 1.4e-37;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VROCHNGGSGYRGFTSTVTGRTQSSWMTPHRHQRTPEPNYDGLTMNYCRNPDADT 60
DB 1 VDCYHGDGQSYRGFTSTVTGRTQSSWMTPHRHQRTPEPNYDGLTMNYCRNPDADK 60

QY 61 GPWCFTTDPISIRWEXCNLTRCSDTEGTV 89
DB 61 GPWCFTTDPISIRWEXCNLTRCSDTEASV 89

RESULT 5

AAB01919 standard; Protein; 192 AA.

AC AAB01919;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringles 4-5 (Val355-Phe546).

XX Plasminogen; human; kringle domain; endothelial cell proliferation;
XX angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
XX antipsoiatric; antiinflammatory; anticancer; antirheumatic; antiarthritic;
XX antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.
 XX
 PR 03-MAY-1996; 96US-0643219.
 PR 03-APR-1997; 97US-0832087.
 XX
 PA (ABBO) ABBOTT LAB.
 PI Davidson DJ;
 XX WPI; 2000-349573/30.
 XX
 DR Preparation of Kringle five peptide fragment for treating various
 XX disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -
 XX
 PS Example 17; Page -: 48pp; English.
 XX
 CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
 CC Syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived
 CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.
 CC
 XX
 SQ Sequence 192 AA;
 Query Match 84.9%; Score 444; DB 21; Length 192;
 Best Local Similarity 82.0%; Pred. No. 1.4e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VROCYNHGNGSYRGTFSTVTYGRTCQSSWSPHRRHQRTPENYPNDGLTNNYCRNPADT 60
 Db 1 VQDCYHGDGSGYRGTSSTTTTGKCCQSSWSPHRRHQRTPENYPNDGLTNNYCRNPADK 60
 QY 61 GPMCFITDPSIRWEYCNLTTRCSDPTGTVV 89
 Db 61 GPMCFITDPSIRWEYCNLTTRCSDPTGTVV 89
 RESULT 6
 ID AAB01905 standard; Protein; 364 AA.
 AC AAB01905;
 XX
 XX 18-SEP-2000 (first entry)
 XX
 DE Human plasminogen kringle 1-4 (angiotensin).
 XX
 XX plasminogen; human; kringle domain; endothelial cell proliferation;
 KM angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KM antiproliferative; antiinflammatory; antiulcer; antithrombotic; antitachycardic;
 KM antiangiogenic; cancer; tumour; autoimmune disease.
 XX
 XX Homo sapiens.
 XX

PN US6057122-A.
 XX
 PD 02-MAY-2000.
 XX
 XX
 PF 05-MAY-1997; 97US-0851350.
 XX
 PR 03-MAY-1996; 96US-0643219.
 PR 03-APR-1997; 97US-0832087.
 XX
 PA (ABBO) ABBOTT LAB.
 PI Davidson DJ;
 XX WPI; 2000-349573/30.
 XX
 DR Preparation of Kringle five peptide fragment for treating various
 XX disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -
 XX
 PS Example 17; Page -: 48pp; English.
 XX
 CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
 CC Syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived
 CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.
 CC
 XX
 SQ Sequence 364 AA;
 Query Match 84.9%; Score 444; DB 21; Length 364;
 Best Local Similarity 82.0%; Pred. No. 2.8e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VROCYNHGNGSYRGTFSTVTYGRTCQSSWSPHRRHQRTPENYPNDGLTNNYCRNPADT 60
 Db 276 VQDCYHGDGSGYRGTSSTTTTGKCCQSSWSPHRRHQRTPENYPNDGLTNNYCRNPADK 335
 QY 61 GPMCFITDPSIRWEYCNLTTRCSDPTGTVV 89
 Db 336 GPMCFITDPSIRWEYCNLTTRCSDPTGTVV 364
 RESULT 7
 ID AAY53868 standard; protein; 369 AA.
 AC AAY53868;
 XX
 XX 13-MAR-2000 (first entry)
 XX
 DE Amino acid sequence of human angiotensin protein.
 XX
 XX Human; plasminogen; angiotensin; greenstatin; thrombolytic factor;
 KM angiogenesis inhibitory protein; proliferation; angiogenesis; cancer;
 KM vascular endothelial cell; ophthalmic disease; glaucoma;
 KM

KW diabetic retinopathy; arthritis; psoriasis.
XX
OS Homo sapiens.
XX
PN MO9961464-A1.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-KR0263.
XX
PR 28-MAY-1998; 98KR-0019535.
PR 27-MAY-1999; 99KR-0019144.
XX
PA (GREC) KOREA GREEN CROSS CORP.
XX
PI You WK, So SH, Ahn BC, Lee H, Jung S, Kim Y, Lee JH, Hong Y;
PI Joe YA, Chang S;
XX
DR WPI; 2000-086703/07.
XX
PT Purifying angiogenesis inhibitors produced as recombinant proteins in
PT Escherichia coli, useful as anticancer agents and for treating ocular
PT diseases -
XX
PS Claim 2; Page 45-47; 55pp; English.
XX
CC The present sequence represents the human angiotatin protein. It
CC is derived from the plasminogen protien, and comprises amino acids
CC 99-467. Greenstatin is also derived from plasminogen, and comprises
CC amino acids 101-354. Angiotatin and greenstatin are used as
CC thrombolytic factors and angiogenesis inhibitory proteins. Angiotatin
CC contains the kringle 1-4 region of plasminogen, and greenstatin contains
CC the kringle 1-3 region of plasminogen. As both proteins contain a high
CC number of disulphide bonds, they are difficult to purify. The
CC specification describes a method for the purification of such
CC angiogenesis inhibitory proteins. The method comprises solubilising
CC the proteins, produced as inclusion bodies in Escherichia coli and
CC refolding the solubilised fraction in buffer containing urea and
CC glutathione. The angiogenesis inhibitory proteins specifically inhibit
CC proliferation of vascular endothelial cells, but not that of
CC non-endothelial cancers or normal cells. The angiogenesis inhibitory
CC proteins are used to suppress angiogenesis, specifically for treating
CC cancers (e.g. of lung, skin and brain) or ophthalmic diseases (e.g.
CC glaucoma and diabetic retinopathy), but also arthritis and psoriasis.
XX
SQ Sequence 369 AA;
XX
Query Match 84.9%; Score 444; DB 21; Length 369;
Best Local Similarity 82.0%; Pred. No. 2.8e-37;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
XX
QY 1 VROCHNGNGOSYRGFTSTVTGRTGOSWSMTPHRHQRTPEPNYDGLTMYCRNPADDT 60
DB 276 VDDCYHGDGOSYRGFTSTVTGRTGOSWSMTPHRHQRTPEPNYDGLTMYCRNPADDT 335
XX
QY 61 GPMCFITDPSIRWEXCNLTRCSDEGTGVV 89
DB 336 GPMCFITDPSIRWEXCNLTRCSDEGTGVV 364
XX
RESULT 8
AAV79226
ID AAV79226 standard; Protein; 374 AA.
XX
AC AAV79226;
XX
DT 19-JUN-2000 (first entry)
XX
DE Angiogenesis inhibitor obtained by plasminogen cleavage.
XX
KW Angiogenesis inhibitor; plasminogen; human; K4 protease;
KW snake venom; cobra; antimetastatic; cytosolic; antitumour; tumour;
KW prostate cancer; breast cancer; colon cancer; lung cancer;
XX

KW leukaemia; metastasis; contraceptive; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 264
FT /note- "N-glycosylated"
XX
PN WO200010506-A2.
XX
PD 02-MAR-2000.
XX
PF 19-AUG-1999; 99WO-US18877.
XX
PR 20-AUG-1998; 98US-0097244.
XX
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
PI Mann KG, Jenny NS;
XX
DR WPI; 2000-246485/21.
XX
PT New angiogenesis inhibitors useful for treating solid tumors,
PT leukemias, tumor metastasis, benign tumor, rheumatoid arthritis,
PT psoriasis and ocular angiogenic diseases -
XX
PS Claim 1; Fig 10; 72pp; English.
XX
CC The present sequence represents a preferred angiogenesis inhibitor
CC of the invention that is obtained by cleavage of human plasminogen
CC with splitting cobra (Naja nigricollis nigricollis) venom K4
CC protease and plasmin. The K4 protease cleaves native plasminogen
CC following amino acid residue 452, with little or no disruption of
CC the first 4 plasminogen kringles. Plasmin cleaves between residues
CC 77 and 78 of human plasminogen. Thus, the present protein spans
CC amino acid residues 78-451 of plasminogen. The angiogenesis
CC inhibitors obtained from plasminogen can be used to inhibit tumour
CC growth in a mammal, preferably human. They are useful for treating
CC angiogenesis-associated diseases such as: solid tumours, prostate
CC cancer, breast cancer, colon cancer and lung cancer (claimed);
CC blood-borne tumors such as leukaemia; metastasis; benign tumours;
CC rheumatoid arthritis; psoriasis; ocular angiogenic diseases;
CC myocardial angiogenesis; plaque neovascularization; telangiectasia;
CC haemophilic joints; angiodioma; wound granulation; excessive or
CC abnormal stimulation of endothelial cells; and as birth control
CC agents by preventing vascularization required for embryo
CC implantation. The inhibitors are administered also to extend the
CC dormancy of micrometastases and to stabilize any residual primary
CC tumour.
XX
SQ Sequence 374 AA;
XX
Query Match 84.9%; Score 444; DB 21; Length 374;
Best Local Similarity 82.0%; Pred. No. 2.9e-37;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
XX
QY 1 VROCHNGNGOSYRGFTSTVTGRTGOSWSMTPHRHQRTPEPNYDGLTMYCRNPADDT 60
DB 277 VDDCYHGDGOSYRGFTSTVTGRTGOSWSMTPHRHQRTPEPNYDGLTMYCRNPADDT 336
XX
QY 61 GPMCFITDPSIRWEXCNLTRCSDEGTGVV 89
DB 337 GPMCFITDPSIRWEXCNLTRCSDEGTGVV 365
XX
RESULT 9
AAV79225
ID AAV79225 standard; Protein; 375 AA.
XX
AC AAV79225;
XX
DT 19-JUN-2000 (first entry)
XX

DE			Angiogenesis inhibitor obtained by plasminogen cleavage.
XX			Angiogenesis inhibitor; plasminogen; human; K4 protease;
KW			snake venom; cobra; antimetastatic; cytostatic; antitumor;
KW			prostate cancer; breast cancer; colon cancer; lung cancer;
KX			leukaemia; metastasis; contraceptive; therapy.
XX			
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	Modified-site	265	
FT	/note-	"N-Glycosylated"	
XX			
PB	WO200010506-A2.		
PD	02-MAR-2000.		
PF	19-AUG-1999;	99WO-US18877.	
PR	20-AUG-1998;	98US-0097244.	
PA	(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.		
PI	Mann KG, Jenny NS;		
DR	WPI; 2000-246485/21.		
PT	New angiogenesis inhibitors useful for treating solid tumors,		
PT	leukemias, tumor metastasis, benign tumor, rheumatoid arthritis,		
PT	psoriasis and ocular angioelectric diseases	-	
PS	Claim 1; Fig 9; 72pp; English.		
XX			
CC	The present sequence represents a preferred angiogenesis inhibitor		
CC	of the invention that is obtained by cleavage of human plasminogen		
CC	with splitting cobra (Naja nigricollis nigricollis) venom K4		
CC	protease and plasmin. The K4 protease cleaves native plasminogen		
CC	following amino acid residue 452, with little or no disruption of		
CC	the first 4 plasminogen kringles. Plasmin cleaves between residues		
CC	77 and 78 of human plasminogen. Thus, the present protein spans		
CC	amino acid residues 77-451 of plasminogen. The angiogenesis		
CC	inhibitors obtained from plasminogen can be used to inhibit tumour		
CC	growth in a mammal, preferably human. They are useful for treating		
CC	angiogenesis-associated diseases such as: solid tumours, prostate		
CC	cancer, breast cancer, colon cancer and lung cancer (claimed);		
CC	blood-borne tumors such as leukemia; metastasis; benign tumours;		
CC	rheumatoid arthritis; psoriasis; ocular angioelectric diseases;		
CC	myocardial arteritis; plaque neovascularization; telangiectasia;		
CC	haemophilic joints; angiodiroma; wound granulation; excessive or		
CC	abnormal stimulation of endothelial cells; and as birth control		
CC	agents by preventing vascularization required for embryo		
CC	implantation. The inhibitors are administered also to extend the		
CC	domancy of micrometastases and to stabilize any residual primary		
CC	tumour.		
XX			
SQ	Sequence	375 AA;	
Query Match		84.9%; Score 444; DB 21; Length 375;	
Best Local Similarity		82.0%; Pred. No. 2.9e-37;	
Matches	73; Conservative	7; Mismatches 9; Indels 0; Gaps 0	
OY	1 VRCVHGNGSQSYRGFTSTVTGTRTQSWSMT PRRHQRTPENY PNDGLTMNYCRNPADT 60		
DB	278 VDDCYHGDQDSYRGTSSTTTGGKKCSQSWSMTPRHHRKQTPEHY PNAAGLTMYCRNPADAK 337		
OY	61 GPWCCTTDPSIRNEYCNLTRCSDTGTV 89		
DB	338 GPWCCTTDPSVRMEYCINLKKCGSTASVV 366		
RESULT 10			
ID	AAM07579 standard; protein; 378 AA.		
	AAM07579		

[illegible]

DE Human angioestatin protein sequence.

XX Angiogenesis-inhibiting protein receptor; angiogenesis; angioestatin;
 XX endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
 KW psoriasis; scleroderma; myocardial angioestatin; Crohn's disease;
 KW cerebral collateral; arteriovenous malformation; rheobiosis; cancer;
 KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
 KW Helicobacter related disease; fracture; cat scratch fever.

XX Homo sapiens.

PN WO200032631-A2.

PD 08-JUN-2000.

XX 06-DEC-1999; 99MO-US28897.

XX 04-DEC-1998; 98US-0206059.

XX (ENTR-) ENTREMED INC.

PI Macdonald NJ, Sim KL;

XX WPI; 2000-412290/35.

XX New angiogenesis-inhibiting protein receptors, useful in methods for
 PT treating diseases and processes that are mediated by angiogenesis, such
 PT as solid tumours, psoriasis, scleroderma and myocardial angioestatin -
 XX Disclosure; Figure 2; 100pp; English.

XX This invention relates to angiogenesis-inhibiting protein receptors, and
 CC the DNA sequences encoding them. Angiogenesis is the generation of new
 CC blood vessels into a tissue, and normally occurs in wound healing,
 CC foetal and embryonal development and the formation of the corpus luteum,
 CC endometrium and placenta. Angioestatin is a protein (see AAB16450 and
 CC AAB6202) involved in angiogenesis, and has an amino acid sequence
 CC similar to that of a plasminogen fragment (see murine plasminogen
 CC AAB16490). Angioestatin has the ability to inhibit angiogenesis.
 CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and
 CC AAB6203). Sequences AAB68242 and AAB16522 represent coding and protein
 CC sequences of human laminin. Laminin is an angioestatin binding protein,
 CC and some of the peptides of the invention share homology with regions of
 CC laminin. Peptides AAB16452-16521 (excluding AAB16490) are the
 CC angioestatin-inhibiting protein receptor fragments of the invention. The
 CC peptides bind either angioestatin or endostatin and can be used in methods
 CC for treating diseases and processes that are mediated by angiogenesis,
 CC such as solid tumours, psoriasis, scleroderma, myocardial angioestatin,
 CC Crohn's disease, cerebral collaterals, arteriovenous malformations,
 CC rheobiosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,
 CC Helicobacter related diseases, fractures, placenta and cat scratch
 CC fever. They are useful for the detection and prognosis of cancer. DNA
 CC sequences A628204-A628241 encode the peptides of the invention.

XX SQ Sequence 378 AA;

Query Match 84.9%; Score 444; DB 21; Length 378;
 Best Local Similarity 82.0%; Pred. No. 2.9e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 1 VROCCHNGGQSYRGFTSTVTGRTGQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DT 60
 Db 282 VQDCYHGGQSYRGFTSTVTGRTGQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DK 341
 61 GPWCFTTDPSSIRWEYCNLTRCSDTGTVV 89
 342 GPWCFTTDPSSIRWEYCNLTRCSDTGTVV 370

RESULT 12
 AAM48894 standard; Protein; 378 AA.

AC AAM48894;

XX 04-APR-2002 (first entry)

DE Human angioestatin protein.

XX Human; angioestatin; endostatin; angiogenesis; cancer; metastasis;
 KW psoriasis; scleroderma; Crohn's disease; corneal disease;
 KW retinopathy; arthritis; wound healing; Helicobacter pylori; peptic ulcer;
 KW gene therapy; angioestatin antagonist; endostatin antagonist;
 KW antiangiogenic; cytosatic; antiarthritic; antiinflammatory;
 KW cerebroprotective; antidiabetic; virucide; antipyretic; vulnerary;
 KW gynaecological; cat scratch fever.

XX Homo sapiens.

PN WO200193897-A2.

PD 13-DEC-2001.

XX 04-JUN-2001; 2001WO-US17947.

XX 02-JUN-2000; 2000US-209065P.

XX 08-MAY-2001; 2001US-289387P.

XX (ENTR-) ENTREMED INC.

PI Sim KL, Macdonald NJ;

XX WPI; 2002-130569/17.

XX Regulating angiogenesis and treatment of angiogenesis-mediated
 PT diseases, e.g. hemangioma, tumors or cancer, by administering a
 PT tropomyosin binding compound or actin disrupting compound -
 XX Disclosure; Fig 2; 95pp; English.

XX The present invention relates to methods of regulating angiogenesis in an
 CC individual by administering an angiogenesis regulating composition
 CC comprising a tropomyosin binding compound or an actin disrupting
 CC compound. The compositions are useful for treating diseases and processes
 CC mediated by angiogenesis including haemangioma, solid tumours, blood
 CC borne tumours, leukaemia, metastasis, Crohn's disease, coronary or
 CC cerebral collaterals, arthritis, diabetic neovascularisation, macular
 CC degeneration, wound healing, Helicobacter related diseases, ovulation,
 CC menstruation, and cat scratch fever. The present sequence is a protein,
 CC described in the exemplification of the invention.

XX SQ Sequence 378 AA;

Query Match 84.9%; Score 444; DB 23; Length 378;
 Best Local Similarity 82.0%; Pred. No. 2.9e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 1 VROCCHNGGQSYRGFTSTVTGRTGQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DT 60
 Db 282 VQDCYHGGQSYRGFTSTVTGRTGQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DK 341
 61 GPWCFTTDPSSIRWEYCNLTRCSDTGTVV 89
 342 GPWCFTTDPSSIRWEYCNLTRCSDTGTVV 370

RESULT 13
 AA02105 standard; Protein; 380 AA.

XX AA02105;

XX 16-JUL-1999 (first entry)

XX A multifunctional protein of the invention.

KM Angiotensin; endostatin; interferon; thrombospondin;
 KM interferon-inducible protein; platelet factor 4; anti-angiogenic;
 KM anti-tumor; multifunctional protein; angiogenic-mediated disease;
 KM cancer; diabetic retinopathy; macular degeneration; arthritis;
 KM tumor cell production.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN MO9916889-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 30-SEP-1998; 98WC-US20464.
 XX
 PR 01-OCT-1997; 97US-0060609.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Bolanowski MA, Caparon MH, Casperson GF, Gregory SA;
 PI Klein BK, McKearn JP;
 DR WPI; 1999-255098/21.
 XX
 PT New multifunctional proteins useful for treating angiogenic-mediated
 PT diseases
 PS
 XX Claim 5; Page 100-101; 121pp; English.
 CC The specification describes multifunctional proteins which comprise
 CC combinations of angiotensin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have
 CC anti-angiogenic and/or anti-tumor activity. The multifunctional protein
 CC may exhibit useful properties such as having similar or greater
 CC biological activity when compared to a single factor or by having
 CC improved half-life or decreased adverse side effects, or a combination
 CC of these properties. The proteins can be used for treating an
 CC angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular
 CC degeneration, or arthritis. They can also be used for inhibiting the
 CC production of tumor cells (characteristic of lung, breast, ovarian,
 CC prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma,
 CC hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor
 CC growth. The present sequence represents a multifunctional protein of the
 CC invention.
 CC
 XX
 SQ Sequence 380 AA;
 XX
 QY Query Match 84.9%; Score 444; DB 20; Length 380;
 Db Best Local Similarity 82.0%; Pred. No. 2.9e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VROCYNHGQSYRGTESTVTYGRTCQSSWMTPHRHQRTPEYNDGLTMNYCRNPADT 60
 Db 284 VQDCHGDSGYRGSTSTTTGKKCSWMTPHRHQRTPEYNDGLTMNYCRNPADK 343
 QY 61 GPMCFITDPSIRWEYCNLTRCSDEGTIV 89
 Db 344 GPMCFITDPSIRWEYCNLTRCSDEGTIV 372
 XX
 RESULT 14
 AAM51457
 ID AAM51457 standard; protein: 437 AA.
 XX
 AC AAM51457;
 XX
 DT 02-SEP-1998 (first entry)
 XX
 DE Human plasminogen fragment with neovascularisation inhibiting activity.
 XX
 KM Human plasminogen; neovascularisation; angiotensin; inhibition;
 KM elastase; Sepharose.
 XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 4..81
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 25..64
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 53..76
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 108..187
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 129..170
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 158..182
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 194..313
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 204..212
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 234..250
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 326..393
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 356..372
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 383..411
 FT Disulfide-bond /label= Disulphide_bond
 XX
 PN JP10158300-A.
 XX
 PD 16-JUN-1998.
 XX
 PF 28-NOV-1996; 96JP-0317250.
 XX
 PR 28-NOV-1996; 96JP-0317250.
 XX
 PA (SUZM) SUZUKI KK.
 XX
 DR WPI; 1998-393476/34.
 XX
 PT Human plasminogen derived polypeptide - has neovascularisation
 PT inhibiting activity
 PS
 XX Claim 1; Page 2; 16pp; Japanese.
 CC The invention relates to a neovascularisation inhibitor which comprises
 CC amino acids 355-791 of human plasminogen. Also claimed are a method for
 CC the preparation of angiotensin, and angiotensin prepared by this method.
 CC The human plasminogen protein fragment is prepared by: (a) applying human
 CC plasminogen to a lysine Sepharose column to separate it into plasminogen
 CC form 1 and form 2; (b) separating plasminogen form 1 and form 2 and
 CC digesting them with elastase; (c) fractionating the elastase-decomposed
 CC product of form 1 plasminogen and form 2 plasminogen in a lysine
 CC Sepharose column; (d) collecting the fractions bound to the lysine
 CC an Aminohexyl Sepharose column; and (e) collecting the fraction bound to
 CC the Aminohexyl Sepharose column. This human plasminogen fragment can be
 CC used to inhibit growth of vascular endothelial cells. The present
 CC sequence represents amino acids 355-791 of human plasminogen.
 CC
 XX
 SQ Sequence 437 AA;
 XX
 QY Query Match 84.9%; Score 444; DB 19; Length 437;
 Db Best Local Similarity 82.0%; Pred. No. 3.4e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VROCYNHGQSYRGTESTVTYGRTCQSSWMTPHRHQRTPEYNDGLTMNYCRNPADT 60
 Db 1 VQDCHGDSGYRGSTSTTTGKKCSWMTPHRHQRTPEYNDGLTMNYCRNPADK 60
 QY 61 GPMCFITDPSIRWEYCNLTRCSDEGTIV 89
 Db 61 GPMCFITDPSIRWEYCNLTRCSDEGTIV 89

RESULT 15

AAV79224
ID AAV79224 standard; Protein; 452 AA.

AC AAV79224;

DT 19-JUN-2000 (first entry)

DE Angiogenesis inhibitor obtained by human plasminogen cleavage.

XX Angiogenesis inhibitor; plasminogen; human; K4 protease;

KW snake venom; cobra; Naja nigricollis nigricollis; metastatic;

KW cytostatic; anticancer; tumour; prostate cancer; breast cancer;

KW colon cancer; lung cancer; leukaemia; metastasis; contraceptive;

XX therapy.

XX Homo sapiens.

XX Key

FT Peptide

FT Cleavage-site

FT Misc-difference

FT Misc-difference

FT Misc-difference

FT Modified-site

FT Modified-site

FT Modified-site

XX WO200010506-A2.

XX 02-MAR-2000.

XX 19-AUG-1999; 99WO-US18877.

XX 20-AUG-1998; 98US-0097244.

XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

XX Mann KG, Jenny NS;

XX WPI; 2000-246485/21.

XX New angiogenesis inhibitors useful for treating solid tumors,

XX leukemias, tumor metastasis, benign tumor, rheumatoid arthritis,

XX psoriasis and ocular angiogenic diseases

XX Claim 14; Fig 8; 72pp; English.

XX The present sequence represents an angiogenesis inhibitor obtained

XX by cleavage of human plasminogen with snake venom K4 protease from

XX splitting cobra (Naja nigricollis nigricollis). The K4 protease

XX cleaves the plasminogen following amino acid residue 452, producing

XX an angiogenesis inhibitor with little or no disruption of the first

XX 4 plasminogen kringles. Further, preferred angiogenesis inhibitors

XX of the invention are obtained by plasmin cleavage of this K4

XX protease-cleaved plasminogen fragment (see AAV79225 and AAV79226). The

XX angiogenesis inhibitors are used for inhibiting tumour growth in a

XX mammal, preferably human. They are useful for treating

XX angiogenesis-associated diseases such as: solid tumours, prostate

XX cancer, breast cancer, colon cancer and lung cancer (claimed);

XX blood-borne tumors such as leukaemia; metastasis; benign tumours;

XX rheumatoid arthritis; psoriasis; ocular angiogenic diseases;

XX myocardial angiogenesis; plaque neovascularization; telangiectasia;

XX haemophilic joints; angiodysplasia; wound granulation; excessive or

XX abnormal stimulation of endothelial cells; and as birth control

CC agents by preventing vascularization required for embryo

CC implantation. The inhibitors are administered also to extend the

CC dormancy of micrometastases and to stabilize any residual primary

CC tumor.

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Sequence 452 AA;

Query Match 84.9%; Score 444; DB 21; Length 452;

Best Local Similarity 82.0%; Pred. No. 3.5e-37;

Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGQSYRGTFSTTTTGTCTCQSWSSMTPHRQRTPENYVNDGLTMYCRNPADT 60

DB 355 VQDCYHGDQSYRGTSSTTTGKCCQSWSSMTPHRQRTPENYVNDGLTMYCRNPADK 414

QY 61 GPWCFTTDPSTIRWECNLTRECSDEGTIV 89

DB 415 GPWCFTTDPSTIRWECNLTRECSDEGTIV 443

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OM protein - protein search, using SW model

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Listing first 45 summaries

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Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	517	98.9	1169	US-09-870-759-126 Sequence 126, App
2	517	98.9	1169	US-09-751-708A-126 Sequence 126, App
3	447	85.5	368	US-09-761-120-42 Sequence 42, Appl
4	447	85.5	368	US-10-402-364-42 Sequence 42, Appl
5	444	84.9	378	US-09-873-676-1 Sequence 1, Appl
6	444	84.9	378	US-09-335-325-42 Sequence 42, Appl
7	444	84.9	391	US-10-131-241-42 Sequence 42, Appl
8	444	84.9	391	US-10-304-287-7 Sequence 7, Appl
9	444	84.9	394	US-10-304-287-8 Sequence 8, Appl
10	444	84.9	458	US-09-946-893-4 Sequence 4, Appl
11	444	84.9	569	US-09-946-893-5 Sequence 5, Appl
12	444	84.9	571	US-09-946-893-8 Sequence 6, Appl
13	444	84.9	576	US-09-946-893-3 Sequence 8, Appl
14	444	84.9	791	US-09-967-386-1 Sequence 1, Appl
15	444	84.9	791	US-10-304-287-1 Sequence 1, Appl

16	444	84.9	810	US-09-946-893-2 Sequence 2, Appl
17	444	84.9	810	US-10-237-144-1 Sequence 1, Appl
18	444	84.9	810	US-10-193-656-2 Sequence 2, Appl
19	435	83.2	363	US-10-292-418-11 Sequence 11, Appl
20	422	80.7	352	US-09-761-120-40 Sequence 40, Appl
21	422	80.7	352	US-09-335-325-40 Sequence 40, Appl
22	422	80.7	352	US-10-402-364-40 Sequence 40, Appl
23	422	80.7	352	US-10-402-364-40 Sequence 40, Appl
24	417	79.7	78	US-09-751-064-5 Sequence 5, Appl
25	417	79.7	78	US-09-761-120-23 Sequence 23, Appl
26	417	79.7	78	US-09-335-325-23 Sequence 23, Appl
27	417	79.7	78	US-10-267-137-9 Sequence 9, Appl
28	417	79.7	78	US-10-402-364-23 Sequence 23, Appl
29	417	79.7	78	US-10-402-364-52 Sequence 52, Appl
30	417	79.7	78	US-10-131-241-23 Sequence 23, Appl
31	413	79.0	451	US-10-157-369-2 Sequence 2, Appl
32	412	78.8	364	US-10-157-369-4 Sequence 4, Appl
33	404	77.2	359	US-10-292-418-40 Sequence 40, Appl
34	400	76.5	378	US-09-761-120-41 Sequence 41, Appl
35	400	76.5	378	US-09-335-325-41 Sequence 41, Appl
36	400	76.5	378	US-10-402-364-41 Sequence 41, Appl
37	400	76.5	378	US-10-131-241-41 Sequence 41, Appl
38	400	76.5	459	US-09-761-120-46 Sequence 46, Appl
39	400	76.5	459	US-10-402-364-46 Sequence 46, Appl
40	400	76.5	812	US-09-788-142-1 Sequence 1, Appl
41	400	76.5	812	US-09-761-120-1 Sequence 1, Appl
42	400	76.5	812	US-09-873-676-81 Sequence 81, Appl
43	400	76.5	812	US-09-335-325-1 Sequence 1, Appl
44	400	76.5	812	US-10-402-364-1 Sequence 1, Appl
45	400	76.5	812	US-10-131-241-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-870-759-126
; Sequence 126, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIORITY FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-126

Query Match 98.9%; Score 517; DB 10; Length 1169;
Best Local Similarity 98.9%; Pred. No. 9e+49; 1; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 1;

QY 1 VRQCHNGGQSYRGFTSTTVGRTGQSSMTPHRHQRTPENYPNDGLTNNYCRNPADT 60
DB 742 VRQCHNGGQSYRGFTSTTVGRTGQSSMTPHRHQRTPENYPNDGLTNNYCRNPADT 801
QY 61 GPWCFTTDPSTIRWEYCNLTRCSDEGTIV 89
DB 802 GPWCFTTDPSTIRWEYCNLTRCSDEGTIV 830

RESULT 2
US-09-751-708A-126
; Sequence 126, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:

```

; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-708A-126

Query Match      98.9%; Score 517; DB 12; Length 1169;
Best Local Similarity 98.9%; Pred. No. 9e-49;
Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VRQCYHNGSGSYRGFTSTVTGRTGSCWSSMTPHRHQRTPEPNYNDGLTMNYCRNPADT 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 742 VRQCYHNGSGSYRGFTSTVTGRTGSCWSSMTPHRHQRTPEPNYNDGLTMNYCRNPADT 801
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 GPCFTTDPsirwEYCNLTkRCSDTEGTVV 89
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 802 GPCFTTDPsirwEYCNLTkRCSDTEGTVV 830
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-09-761-120-42
; Sequence 42, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05940-0151 (43171-252068)
; CURRENT APPLICATION NUMBER: US/09/761,120
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Kringle 1-4 BKLS
US-09-761-120-42

Query Match      85.5%; Score 447; DB 9; Length 368;
Best Local Similarity 82.0%; Pred. No. 1.5e-41;
Matches 73; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 VRQCYHNGSGSYRGFTSTVTGRTGSCWSSMTPHRHQRTPEPNYNDGLTMNYCRNPADT 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 272 VQDCYHGDQSYRGFTSTTTGKCKQSWSSMTPHRHQKTPENYPNAGLTMYCRNPADK 331
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 GPCFTTDPsirwEYCNLTkRCSDTEGTVV 89
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 332 GPCFTTDPsirwEYCNLTkRCSDTEASVV 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-10-402-364-42
; Sequence 42, Application US/10402364
; Publication No. US20040002459A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael
```

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; APPLICANT: Folkman, M. Judah
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05213-2151 (43170-252068)
; CURRENT APPLICATION NUMBER: US/10/402,364
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/761,120A
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Kringle 1-4 BKLS
US-10-402-364-42

Query Match      85.5%; Score 447; DB 12; Length 368;
Best Local Similarity 82.0%; Pred. No. 1.5e-41;
Matches 73; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 VRQCYHNGSGSYRGFTSTVTGRTGSCWSSMTPHRHQRTPEPNYNDGLTMNYCRNPADT 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 272 VQDCYHGDQSYRGFTSTTTGKCKQSWSSMTPHRHQKTPENYPNAGLTMYCRNPADK 331
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 GPCFTTDPsirwEYCNLTkRCSDTEGTVV 89
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 332 GPCFTTDPsirwEYCNLTkRCSDTEASVV 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-09-873-676-1
; Sequence 1, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-676-1

Query Match      84.9%; Score 444; DB 9; Length 378;
Best Local Similarity 82.0%; Pred. No. 3.4e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VRQCYHNGSGSYRGFTSTVTGRTGSCWSSMTPHRHQRTPEPNYNDGLTMNYCRNPADT 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 282 VQDCYHGDQSYRGFTSTTTGKCKQSWSSMTPHRHQKTPENYPNAGLTMYCRNPADK 341
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 GPCFTTDPsirwEYCNLTkRCSDTEGTVV 89
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 342 GPCFTTDPsirwEYCNLTkRCSDTEASVV 370
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
US-09-335-325-42
```

Sequence 42, Application US/09335325
Patent No. US2002016471A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reilly, Michael
Sim, B. Kim Lee
Cao, Yihai
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
City: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K1-48L5
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-335-325-42
Query Match 84.9%; Score 444; DB 10; Length 378;
Best Local Similarity 82.0%; Pred. No. 3.4e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 VROCHNGGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT 60
DB 282 VDDCYHGDGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADK 341
QY 61 GPMCFITDPSIRWEYCNLTRCSDFTEGTV 89
DB 342 GPMCFITDPSIRWEYCNLTRCSDFTEASV 370
RESULT 7
US-10-131-241-42
Sequence 42, Application US/10131241
Publication No. US20030012792A1
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 42
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-241-42
Query Match 84.9%; Score 444; DB 15; Length 378;
Best Local Similarity 82.0%; Pred. No. 3.4e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 VROCHNGGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT 60
DB 282 VDDCYHGDGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADK 341
QY 61 GPMCFITDPSIRWEYCNLTRCSDFTEGTV 89
DB 342 GPMCFITDPSIRWEYCNLTRCSDFTEASV 370
RESULT 8
US-10-304-287-7
Sequence 7, Application US/10304287
Publication No. US20030083234A1
GENERAL INFORMATION:
APPLICANT: Waisman, David M.
TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
FILE REFERENCE: ME02-001
CURRENT APPLICATION NUMBER: US/10/304,287
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 60/333,866
PRIOR FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Word
SEQ ID NO 7
LENGTH: 391
TYPE: PRT
ORGANISM: mammalian
US-10-304-287-7
Query Match 84.9%; Score 444; DB 15; Length 391;
Best Local Similarity 82.0%; Pred. No. 3.5e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 VROCHNGGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT 60
DB 278 VDDCYHGDGQSYRGFTSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADK 337
QY 61 GPMCFITDPSIRWEYCNLTRCSDFTEGTV 89
DB 338 GPMCFITDPSIRWEYCNLTRCSDFTEASV 366
RESULT 9
US-10-304-287-8
Sequence 8, Application US/10304287
Publication No. US20030083234A1
GENERAL INFORMATION:
APPLICANT: Waisman, David M.
APPLICANT: Kwon, Mijung
TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor

```
FILE REFERENCE: ME02-001
CURRENT APPLICATION NUMBER: US/10/304,287
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 60/333,866
PRIOR FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Word
SEQ ID NO 8
LENGTH: 394
TYPE: PRT
ORGANISM: mammalian
US-10-304-287-8

Query Match
Best Local Similarity 84.9%; Score 444; DB 15; Length 394;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRCCYHNGSGSYRGFTSTVTYGRTCQSWSSMTPHRHQRTPEYPNNDGLTMNYCRNPDA DT 60
DB 278 VQDCYHGDGQSYRGFTSTVTYGRTCQSWSSMTPHRHQRTPEYPNNDGLTMNYCRNPDA DT 337
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 338 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 366

RESULT 10
US-09-946-893-4
Sequence 4, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
FILE REFERENCE: Newburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,893
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
US-09-946-893-4

Query Match
Best Local Similarity 84.9%; Score 444; DB 9; Length 458;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRCCYHNGSGSYRGFTSTVTYGRTCQSWSSMTPHRHQRTPEYPNNDGLTMNYCRNPDA DT 60
DB 272 VQDCYHGDGQSYRGFTSTVTYGRTCQSWSSMTPHRHQRTPEYPNNDGLTMNYCRNPDA DT 331
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 332 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 360

RESULT 11
US-09-946-893-5
Sequence 5, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
FILE REFERENCE: Newburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,893
PRIOR FILING DATE: 2000-09-05
```

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NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 569
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
US-09-946-893-5

Query Match
Best Local Similarity 84.9%; Score 444; DB 9; Length 569;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRCCYHNGSGSYRGFTSTVTYGRTCQSWSSMTPHRHQRTPEYPNNDGLTMNYCRNPDA DT 60
DB 374 VQDCYHGDGQSYRGFTSTVTYGRTCQSWSSMTPHRHQRTPEYPNNDGLTMNYCRNPDA DT 433
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 434 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 462

RESULT 12
US-09-946-893-8
Sequence 8, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
FILE REFERENCE: Newburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,893
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 571
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
US-09-946-893-8

Query Match
Best Local Similarity 84.9%; Score 444; DB 9; Length 571;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRCCYHNGSGSYRGFTSTVTYGRTCQSWSSMTPHRHQRTPEYPNNDGLTMNYCRNPDA DT 60
DB 374 VQDCYHGDGQSYRGFTSTVTYGRTCQSWSSMTPHRHQRTPEYPNNDGLTMNYCRNPDA DT 433
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 434 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 462

RESULT 13
US-09-946-893-6
Sequence 6, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
FILE REFERENCE: Newburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,893
PRIOR FILING DATE: 2000-09-05
```

NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 576
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
OTHER INFORMATION: with a tumor targeting signal
US-09-946-893-6

Query Match 84.9%; Score 444; DB 9; Length 576;
Best Local Similarity 82.0%; Pred. No. 5.4e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGQSYRGTSYTTGRTQSWSSMTPHRQRTPEPNYNDGLTMNYCRNPADT 60
DB 374 VQDCYHGDQSYRGTSYTTGRTQSWSSMTPHRQRTPEPNYNDGLTMNYCRNPADK 433

QY 61 GPWCFTTDPISIRWEYCNLTRCSDTEGTV 89
DB 434 GPWCFTTDPISIRWEYCNLKKCSGTEASV 462

RESULT 14
US-09-967-386-1
Sequence 1, Application US/09967386
Patent No. US2002015992A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Henkin, Jack
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
FILE REFERENCE: 6738-US-02
CURRENT APPLICATION NUMBER: US/09/967,386
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/236,550
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 791
TYPE: PRT
ORGANISM: Homo sapiens
US-09-967-386-1

Query Match 84.9%; Score 444; DB 10; Length 791;
Best Local Similarity 82.0%; Pred. No. 7.6e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGQSYRGTSYTTGRTQSWSSMTPHRQRTPEPNYNDGLTMNYCRNPADT 60
DB 355 VQDCYHGDQSYRGTSYTTGRTQSWSSMTPHRQRTPEPNYNDGLTMNYCRNPADK 414

QY 61 GPWCFTTDPISIRWEYCNLTRCSDTEGTV 89
DB 415 GPWCFTTDPISIRWEYCNLKKCSGTEASV 443

RESULT 15
US-10-304-287-1
Sequence 1, Application US/10304287
Publication No. US20030083234A1
GENERAL INFORMATION:
APPLICANT: Waleman, David M.
APPLICANT: Kwon, Mijung
TITLE OF INVENTION: Anti angiogenesis methods, compositions and uses therefor
FILE REFERENCE: ME02-001
CURRENT APPLICATION NUMBER: US/10/304,287
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 60/333,866
PRIOR FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Word
SEQ ID NO 1
LENGTH: 791
TYPE: PRT
ORGANISM: mammalian
US-10-304-287-1

Query Match 84.9%; Score 444; DB 15; Length 791;
Best Local Similarity 82.0%; Pred. No. 7.6e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGQSYRGTSYTTGRTQSWSSMTPHRQRTPEPNYNDGLTMNYCRNPADT 60
DB 355 VQDCYHGDQSYRGTSYTTGRTQSWSSMTPHRQRTPEPNYNDGLTMNYCRNPADK 414

QY 61 GPWCFTTDPISIRWEYCNLTRCSDTEGTV 89
DB 415 GPWCFTTDPISIRWEYCNLKKCSGTEASV 443

Search completed: January 12, 2004, 17:29:39
Job time: 26.0977 secs

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 2
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: angiogenesis inhibitor
NAME/KEY: MOD RES
LOCATION: (265)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-2

Query Match 84.9%; Score 444; DB 4; Length 375;
Best Local Similarity 82.0%; Pred. No. 1.8e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Db 278 VQDCYHGDGQSYRGTSSTTTTGKCCQSSMTPHRQKTPENYPMGLTMYCRNPDAK 337
QY 61 GPMCFITDPSIRWEYCNLTRCSPTGCTV 89
Db 338 GPMCFITDPSIRWEYCNLTRCSPTGCTV 366

RESULT 3
US-08-612-788-42
Sequence 42, Application US/08612788
Patent No. 5837682
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3799
TELEFAX: 404-818-3700
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:

CLONE: K1-4BKLS
US-08-612-788-42

Query Match 84.9%; Score 444; DB 2; Length 378;
Best Local Similarity 82.0%; Pred. No. 1.8e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VQDCYHGDGQSYRGTSSTTTTGKCCQSSMTPHRQKTPENYPMGLTMYCRNPDAK 60
Db 282 VQDCYHGDGQSYRGTSSTTTTGKCCQSSMTPHRQKTPENYPMGLTMYCRNPDAK 341
QY 61 GPMCFITDPSIRWEYCNLTRCSPTGCTV 89
Db 342 GPMCFITDPSIRWEYCNLTRCSPTGCTV 370

RESULT 4
US-09-066-028-42
Sequence 42, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K1-4BKLS
US-09-066-028-42

Query Match 84.9%; Score 444; DB 3; Length 378;
Best Local Similarity 82.0%; Pred. No. 1.8e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VRQCHNGQSYRGTFSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPADT 60
Db 282 VQDCYHGDQSYRGTSSTTTGKKCSWSSMTPHRHQRTPENYPNAGLTMNYCRNPADK 341
Qy 61 GPMCFITDPSIRWEXCNLTRCSDTGTVV 89
Db 342 GPMCFITDPSIRWEXCNLTRCSDTGTVV 370

RESULT 5

US-09-206-059-1
Sequence 1, Application US/09206059
Patent No. 6201104
GENERAL INFORMATION:
APPLICANT: Macdonald, Nicholas
APPLICANT: Sim, Kim Lee
TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and
FILE REFERENCE: 05213-0370
CURRENT APPLICATION NUMBER: US/09/206,059
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-09-206-059-1

Query Match 84.9%; Score 444; DB 3; Length 378;
Best Local Similarity 82.0%; Pred. No. 1.8e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VRQCHNGQSYRGTFSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPADT 60
Db 282 VQDCYHGDQSYRGTSSTTTGKKCSWSSMTPHRHQRTPENYPNAGLTMNYCRNPADK 341

Qy 61 GPMCFITDPSIRWEXCNLTRCSDTGTVV 89
Db 342 GPMCFITDPSIRWEXCNLTRCSDTGTVV 370

RESULT 6

US-09-335-325-42
Sequence 42, Application US/09335325
Patent No. 6521439
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reilly, Michael
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K1-4BKLS
SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-09-335-325-42

Query Match 84.9%; Score 444; DB 4; Length 378;
Best Local Similarity 82.0%; Pred. No. 1.8e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VRQCHNGQSYRGTFSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPADT 60
Db 282 VQDCYHGDQSYRGTSSTTTGKKCSWSSMTPHRHQRTPENYPNAGLTMNYCRNPADK 341

Qy 61 GPMCFITDPSIRWEXCNLTRCSDTGTVV 89
Db 342 GPMCFITDPSIRWEXCNLTRCSDTGTVV 370

RESULT 7

US-09-377-250-1
Sequence 1, Application US/09377250
Patent No. 6363364
GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
APPLICANT: SWORDS JENNY, NANCY
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
FILE REFERENCE: 48409/360
CURRENT APPLICATION NUMBER: US/09/377,250
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: plasminogen fragment
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (53)
OTHER INFORMATION: Xaa = Gln or Glu
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (341)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-1

Query Match 84.9%; Score 444; DB 4; Length 451;
Best Local Similarity 82.0%; Pred. No. 2.2e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VRQCHNGQSYRGTFSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMNYCRNPADT 60
Db 354 VQDCYHGDQSYRGTSSTTTGKKCSWSSMTPHRHQRTPENYPNAGLTMNYCRNPADK 413

QY 61 GPMCTTDPBSIRWEYCNLTRCSDEGTGVV 89
DB 414 GPMCTTDPBSVRWEYCNLKKCSGTEASVV 442

RESULT 8

US-09-377-250-4
Sequence 4, Application US/09377250
Patent No. 635364
GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
FILE REFERENCE: 48409/360
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 452
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: plasminogen fragment
NAME/KEY: MOD RES
LOCATION: (53)
OTHER INFORMATION: Xaa = Gln or Glu
FEATURE:
NAME/KEY: MOD RES
LOCATION: (342)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-4

Query Match 84.9%; Score 444; DB 4; Length 452;
Best Local Similarity 82.0%; Pred. No. 2,2e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VROCCHNGSGYRGFTSTVTGRTCCSSMTPHRHQRTPEYVNDGLTMNYCRNPADT 60
DB 355 VODCYHDDQSYRGSTSTTTTGKCCQSSMTPHRHQRTPEYVNDGLTMNYCRNPADK 414
QY 61 GPMCTTDPBSIRWEYCNLTRCSDEGTGVV 89
DB 415 GPMCTTDPBSVRWEYCNLKKCSGTEASVV 443

RESULT 9

US-08-469-486-54
Sequence 54, Application US/08469486
Patent No. 573281
GENERAL INFORMATION:
APPLICANT: Thogersen, Hans Christian
APPLICANT: Holte, Thor Laas
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486

FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906

INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-54

Query Match 84.9%; Score 444; DB 1; Length 790;
Best Local Similarity 82.0%; Pred. No. 4,4e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VROCCHNGSGYRGFTSTVTGRTCCSSMTPHRHQRTPEYVNDGLTMNYCRNPADT 60
DB 354 VODCYHDDQSYRGSTSTTTTGKCCQSSMTPHRHQRTPEYVNDGLTMNYCRNPADK 413
QY 61 GPMCTTDPBSIRWEYCNLTRCSDEGTGVV 89
DB 414 GPMCTTDPBSVRWEYCNLKKCSGTEASVV 442

RESULT 10

US-08-469-658-54
Sequence 54, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Thogersen, Hans Christian
APPLICANT: Holte, Thor Laas
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070

; Patent No. 5981484

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:19:12 : Search time 11.6391 Seconds
(without alignments)
710.580 Million cell updates/sec

Title: US-10-088-548-8
Perfect score: 508
Sequence: 1 EDDCMGNGKGYRGKATTV.....YTMNPKLFDYCDIPICASS 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the chance being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508	100.0	4548	1 S00657	apoprotein(a) (EC
2	432	85.0	810	2 B30848	plasmin (EC 3.4.21
3	430	84.6	810	1 PLHU	plasmin (EC 3.4.21
4	416	81.9	460	2 B61545	plasmin (EC 3.4.21
5	415	81.7	455	2 A61545	plasmin (EC 3.4.21
6	409	80.5	790	1 PLRG	plasmin (EC 3.4.21
7	406	79.9	812	1 PLMS	plasmin (EC 3.4.21
8	406	79.9	812	1 PLBO	plasmin (EC 3.4.21
9	388	76.4	810	2 I46260	plasmin (EC 3.4.21
10	243.5	47.9	169	2 A40522	plasmin (EC 3.4.21
11	243.5	47.9	716	1 JCS61	macrophage-stimula
12	242	47.6	123	2 C61545	plasmin (EC 3.4.21
13	241.5	47.5	711	1 A47136	macrophage-stimula
14	239.5	47.1	716	1 A40332	macrophage-stimula
15	239	47.0	2869	2 T18518	apolipoprotein(a)
16	237.5	46.8	710	1 I51283	apolipoprotein(a)
17	236	46.5	1420	2 A32869	apolipoprotein(a)
18	234.5	46.2	728	1 JH0579	hepatocyte growth
19	228	44.9	120	2 B61545	plasmin (EC 3.4.21
20	227.5	44.8	728	1 A35644	hepatocyte growth
21	227.5	44.8	728	1 A60185	hepatocyte growth
22	213	41.9	89	2 A60140	plasmin (EC 3.4.21
23	206.5	40.6	625	1 TBBO	chrombin (EC 3.4.2
24	206	40.6	411	2 I51285	hepatocyte growth
25	199.5	39.3	336	2 S3879	plasmin precursor
26	198.5	39.1	3	2 B45082	neurotrophic recep
27	195	38.4	617	2 S10511	chrombin (EC 3.4.2
28	191.5	37.7	622	1 TBHU	chrombin (EC 3.4.2
29	187	36.8	562	1 UKHUT	c-plasminogen acti

30	184	36.2	618	2 A35827	thrombin (EC 3.4.2
31	178.5	35.1	615	1 KFU12	coagulation factor
32	174.5	34.4	946	1 A47299	ror-related recept
33	165.5	32.6	603	2 S28941	coagulation factor
34	163.5	32.2	558	2 UC5878	plasma hyaluronan-
35	163.5	32.2	937	2 A45082	neurotrophic recep
36	160	31.5	559	1 A29941	t-plasminogen acci
37	154	30.3	559	1 A35029	t-plasminogen acci
38	154	30.3	655	1 A46688	hepatocyte growth
39	146	28.7	442	1 UKRS	u-plasminogen acci
40	143	28.1	433	1 UKRS	u-plasminogen acci
41	142.5	28.1	560	1 JC4795	plasma hyaluronan-
42	142	28.0	685	1 A48289	neurotrophic recep
43	140	27.6	806	2 T18840	hypothetical prote
44	139.5	27.5	593	2 S45281	coagulation factor
45	138	27.2	432	1 S18932	u-plasminogen acci

ALIGNMENTS

RESULT 1
S00657
apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 08-Dec-2000
C/Accession: S00657; A28017; A47277; 160906; A47233; 152415; 165286
R/McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Pless, G.M.; Scan
Nature 330, 132-137, 1987
A>Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A/Reference number: S00657; MUID:88039109; PMID:3670400
A/Accession: S00657
A/Molecule type: mRNA
A/Residues: 1-4548 <MCU>
A/Cross-references: GB:X06290; EMBL:X06696; NID:928619; PIDN:CAA29618.1; PID:928620
R/Bacon, D.L.; Pless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.;
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A>Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A/Reference number: A28017; MUID:87204109; PMID:3472206
A/Accession: A28017
A/Molecule type: Protein
A/Residues: 20-21, 'P', 23-34, 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200, 292-314, 'W', 316-318
X', 4396-4401 <EAT>
R/Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A>Title: 5' control regions of the apolipoprotein(a) gene and members of the related pla
A/Reference number: A47277; MUID:93165698; PMID:7679504
A/Accession: A47277
A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RES>
A/Cross-references: GB:L07899; NID:9967973; PID:9967974
R/Malaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Saccor
Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A>Title: Characterization by yeast artificial chromosome cloning of the linked apolipop
A/Reference number: A47233; MUID:93087573; PMID:1454851
A/Accession: A47233
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RE2>
A/Cross-references: GB:M90078; NID:9178786; PIDN:AAA35547.1; PID:9553188
A/Note: apo(a) gene 1 (nomenclature of reference 152415)
A/Accession: A47233
A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RES>
A/Cross-references: GB:M90079; NID:9178784; PIDN:AAA35546.1; PID:9553187
R/Jichnose, A.
Biochemistry 31, 3113-3118, 1992
A>Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated wit
A/Reference number: 152415; MUID:92207924; PMID:1554698
A/Accession: 152415

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RB3>
A:Cross-references: GB:M66877; NID:gi78780; PIDN:AA049909.1; PID:G553185
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: I65286
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RB4>
A:Cross-references: GB:M66878; NID:gi78782; PIDN:AA051749.1; PID:G553166
A:Gene: GDB:LPA
A:Genetics:
A:Cross-references: GDB:120699; OMIM:152200
A:Map position: 6q26-q27
A:Note: several genes closely linked on chromosome 6 are identical in the first coding
re of kringle repeats
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C:Keywords: hydrolase; Kringle; lipid binding; lipoprotein; serine proteinase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-45/8/Product: apolipoprotein(a) #status experimental <MAT>
F:28-105/Domain: kringle homology <KR1>
F:142-219/Domain: kringle homology <KR2>
F:255-333/Domain: kringle homology <KR3>
F:370-447/Domain: kringle homology <KR4>
F:484-561/Domain: kringle homology <KR5>
F:598-675/Domain: kringle homology <KR6>
F:712-789/Domain: kringle homology <KR7>
F:825-903/Domain: kringle homology <KR7>
F:940-1017/Domain: kringle homology <KR9>
F:1054-1131/Domain: kringle homology <KR10>
F:1168-1245/Domain: kringle homology <KR11>
F:1282-1359/Domain: kringle homology <KR12>
F:1396-1473/Domain: kringle homology <KR13>
F:1510-1587/Domain: kringle homology <KR14>
F:1624-1701/Domain: kringle homology <KR15>
F:1738-1815/Domain: kringle homology <KR16>
F:1852-1929/Domain: kringle homology <KR17>
F:1966-2043/Domain: kringle homology <KR18>
F:2080-2157/Domain: kringle homology <KR19>
F:2194-2271/Domain: kringle homology <KR20>
F:2308-2385/Domain: kringle homology <KR21>
F:2422-2499/Domain: kringle homology <KR22>
F:2536-2613/Domain: kringle homology <KR23>
F:2650-2727/Domain: kringle homology <KR24>
F:2764-2841/Domain: kringle homology <KR25>
F:2878-2955/Domain: kringle homology <KR26>
F:2992-3069/Domain: kringle homology <KR27>
F:3106-3183/Domain: kringle homology <KR28>
F:3220-3297/Domain: kringle homology <KR29>
F:3334-3411/Domain: kringle homology <KR30>
F:3448-3525/Domain: kringle homology <KR31>
F:3562-3639/Domain: kringle homology <KR32>
F:3767-3853/Domain: kringle homology <KR33>
F:3782-3859/Domain: kringle homology <KR34>
F:3896-3973/Domain: kringle homology <KR35>
F:4010-4087/Domain: kringle homology <KR36>
F:4124-4201/Domain: kringle homology <KR37>
F:4228-4307/Domain: kringle homology <KR38>
F:4328-4541/Domain: trypsin homology <TRY>

RESULT 2
B30848
plasmin (EC 3.4.21.7) precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C:Accession: B32869; B30848
R:Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A:Reference number: B32869; MUID:89174660; PMID:2925543
A:Accession: B32869
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-810 <TON>
A:Cross-references: GB:J04697; NID:g342272; PIDN:AAA6901.1; PID:g342273
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: fibrinolysis; glycoprotein; hydrolyase; kringle; serine proteinase
F:1-86/Domain: plasminogen-related protein precursor homology <PLPH>
F:1-9/Domain: signal sequence #status predicted <SIG>
F:103-181/Domain: kringle homology <KR1>
F:185-262/Domain: kringle homology <KR2>
F:275-352/Domain: kringle homology <KR3>
F:377-454/Domain: kringle homology <KR4>
F:481-560/Domain: kringle homology <KR5>
F:581-803/Domain: trypsin homology <TRY>
F:49-73, 53-61, 103-181, 124-164, 152-176, 185-262, 188-316, 206-245, 234-257, 275-352, 296-335, 324-404/Domain: #status predicted
F:622, 665, 760/Active site: His, Asp, Ser #status predicted

[illegible]

RESULT 3

PLHM
plasmin (EC 3.4.21.7) precursor [validated] - human
NAlternate names: plasminogen precursor [nismomel]
NCOntains: angiotatin; microplasmnin; plasminogen
CSpecies: Homo sapiens (man)
CDate: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
CAccession: A55229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A04646;
R.Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A>Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolysis system
A.Reference number: A55229; PMID:90202879; PMID:2318848
A.Accession: A55229
A:Molecule type: DNA
A.Residues: 1-810 <P&T>
A.Cross-references: GB:J05286; GB:M34276; NID:9190064; PIDN:AAA6013.1; PID:g387026
A:Experimental source: leukocyte; lung fibroblast
R.Margaretta, N.; Bruno, D.; Fontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Tarantini, R.
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A>Title: Definition of the transcription initiation site of human plasminogen gene in liver tissue
A.Reference number: I52242; PMID:91097523; PMID:2268308
A.Accession: I52242
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A.Residues: 1-16 <MALI>
A.Cross-references: GB:M62890; NID:9190092; PIDN:AAA6454.1; PID:g553613
R.Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A>Title: Molecular cloning and characterization of a full-length cDNA clone for human plasminogen activator
A.Accession: A26646; PMID:87162490; PMID:30300813

A:Molecule type: mRNA
 A:Residues: 1-471,'D',473-810 <FOR>
 A:Cross-references: GB:X05199; NID:935530; PIDN:CAA28831.1; PID:935531
 A:Experimental source: liver
 R:Wallinowski, D.P.; Sadler, J.E.; Davie, E.W.
 Biochemistry 23, 4243-4250, 1984
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and
 A:Reference number: 145961; PMID:85023311; PMID:6148961
 A:Accession: 162738
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 292-471,'D',473-810 <MAL2>
 A:Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031
 A:Accession: 184609
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 367-419 <MAL3>
 A:Cross-references: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:9190111
 R:Brumsholtz, R.A.; Lerch, P.G.; Schallier, J.; Rickli, E.E.; Leigler, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1991
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
 A:Reference number: S03735; PMID:81212097; PMID:7238497
 A:Accession: S03735
 A:Molecule type: protein
 A:Residues: 20-71,'E',73-76 <BRU>
 R:Scott-Jensen, L.; Petersen, T.E.; Magnusson, S.
 submitted to the Atlas July 1977
 A:Reference number: A00929
 A:Accession: A00929
 A:Molecule type: protein
 A:Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
 R:Wiman, B.
 Eur. J. Biochem. 76, 129-137, 1977
 A:Title: Primary structure of the B-chain of human plasmin.
 A:Reference number: A04627; PMID:7725245; PMID:142009
 A:Accession: A04627
 A:Molecule type: protein
 A:Residues: 581-810 <W1>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 50, 489-494, 1975
 A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla
 A:Reference number: A04625; PMID:75093329; PMID:122932
 A:Accession: A04625
 A:Molecule type: protein
 A:Residues: 20-50,'Q',51-71,'E',73-85,87-100 <W12>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 58, 539-547, 1975
 A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha
 A:Reference number: A04626; PMID:76043692; PMID:126863
 A:Accession: A04626
 A:Molecule type: protein
 A:Residues: 483-507,'E',509-604 <W13>
 R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
 J. Biol. Chem. 248, 1631-1633, 1973
 A:Title: The primary structure of human plasminogen. II. The histidine loop of human pla
 A:Reference number: A92125; PMID:7319248; PMID:4694729
 A:Accession: A92125
 A:Contents: annotation; active site
 R:Grookopf, W.R.; Summaria, L.; Robbins, K.C.
 J. Biol. Chem. 244, 3590-3597, 1969
 A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
 A:Reference number: A92048; PMID:69234739; PMID:4240117
 A:Accession: A92048
 A:Contents: annotation; active site
 R:Trexlter, M.; Vail, Z.; Patsy, L.
 J. Biol. Chem. 257, 7401-7406, 1982
 A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
 A:Reference number: A92382; PMID:82213905; PMID:6919539
 A:Accession: A92382
 A:Contents: annotation; omega-aminocarboxylic acid binding sites
 R:Vail, Z.; Patsy, L.
 J. Biol. Chem. 259, 13690-13694, 1984
 A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
 A:Reference number: A92458; PMID:85054794; PMID:6094526
 A:Accession: A92458
 A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site

R:Caio, Y.; Ji, R.W.; Davidson, D.; Schallier, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
 J. Biol. Chem. 271, 29461-29467, 1996
 A:Title: Kringle domains of human angiotensin. Characterization of the anti-proliferative
 A:Reference number: A58811; PMID:97067211; PMID:8910613
 A:Accession: A58811
 A:Contents: annotation
 R:Jilinen, H.R.; Uggua, F.; Bini, A.; Collen, D.
 Biochemistry 37, 4699-4702, 1998
 A:Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M
 A:Reference number: A58812; PMID:9548733; PMID:9548733
 A:Accession: A58812
 A:Contents: annotation
 R:Tulinaky, A.; Mulichak, A.M.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51341; PDB:1PK4
 A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
 R:Tulinaky, A.; Wu, T.P.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51486; PDB:1PK4
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
 R:Wu, T.P.; Tulinaky, A.
 submitted to the Brookhaven Protein Data Bank, August 1993
 A:Reference number: A51911; PDB:1PKR
 A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
 R:Padanabhan, K.; Tulinaky, A.
 submitted to the Brookhaven Protein Data Bank, April 1994
 A:Reference number: A52408; PDB:1PKM
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
 R:Tulinaky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995
 A:Reference number: A5244; PDB:1CEA
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 R:Tulinaky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995
 A:Reference number: A5245; PDB:1CEB
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 R:Mulichak, A.M.; Tulinaky, A.; Ravichandran, K.G.
 Biochemistry 30, 10576-10588, 1991
 A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 A
 A:Reference number: A58819; PMID:92031502; PMID:1657148
 A:Accession: A58819
 A:Contents: annotation
 R:Wu, T.P.; Padanabhan, K.; Tulinaky, A.; Mulichak, A.M.
 Biochemistry 30, 10589-10594, 1991
 A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
 A:Reference number: A58818; PMID:92031503; PMID:1657149
 A:Accession: A58818
 A:Contents: annotation
 R:de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padanabhan, K.; Tulinaky, A.; Westbrook, M.I.
 Biochemistry 31, 270-279, 1992
 A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4
 A:Reference number: A39483; PMID:9211803; PMID:1310033
 A:Accession: A39483
 A:Contents: annotation; X-ray crystallography, 2.4 angstroms
 R:Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
 submitted to the Brookhaven Protein Data Bank, June 1995
 A:Reference number: A65980; PDB:1KRN
 A:Accession: A65980
 A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
 R:Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65804; PDB:1HPK
 A:Accession: A65804
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
 R:Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65803; PDB:1HPJ
 A:Accession: A65803
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
 R:Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65804; PDB:1HPK
 A:Accession: A65804
 A:Contents: annotation; conformation by (1)H-NMR, residues 96-184
 R:Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65817; PMID:94237158; PMID:8181476
 A:Accession: A65817
 A:Contents: annotation; conformation by (1)H-NMR
 C:Comment: plasminogen is synthesized by the kidney and is present in plasma and many oti
 C:Comment: plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU at

d PIR:FGHUB).

C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITRHA2) immediately after 580, resulting in two chains connected by two disulfide bonds. Without the inhibitor.

C:Comment: Microplasmin is formed by autocatalytic cleavage of plasmin under artificial conditions.

C:Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. To

C:Gene: GDB:PLG

A:Cross-references: GDB:119498; OMIM:173350

A:Map position: 6q26-q27

A:Intons: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529

C:Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the graafian follicle; also activates the urokinase-type plasminogen act

A:Pathway: fibrinolysis

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-810/Product: plasminogen #status experimental <PRO>

F:20-96/Domain: activation peptide #status experimental <APT>

F:79-466/Product: angiotensin #status experimental <AST>

F:97-580/Domain: plasmin chain A #status experimental <CHA>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:377-454/Domain: kringle homology <KR4>

F:481-560/Domain: kringle homology <KR5>

F:550-580,581-810/Product: microplasmin #status experimental <MNT>

Query Match 84.6%; Score 430; DB 1; Length 810;
Best Local Similarity 82.4%; Pred. No. 1,7e-38;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EODCMFNGKGYRGKATVTGTPCOEWAQEPHRSFTPGTNKWAQLEKNYCRNPDG 60
Db 478 EEDCMFNGKGYRGKATVTGTPCOEWAQEPHRSFTPGTNKWAQLEKNYCRNPDG 537

Qy 61 INGPWCYTNNPKRLFDYCDIPLCASS 85
Db 538 VGGPWCYTNNPKRLFDYCDIPLCASS 562

RESULT 4

B61545

plasmin (EC 3.4.21.7) precursor - sheep (fragments)

N:Alternate names: plasminogen

N:Contains: miniplasminogen

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999

C:Accession: B61545; S28200

R:Schaller, U.; Rickli, E.E.

Enzyme 40, 63-69, 1988

A:Title: Structural aspects of the plasminogen of various species.

A:Reference number: A61545; MUID:8905015; PMID:3168975

A:Accession: B61545

A:Molecule type: protein

A:Residues: 1-37,38-117 <SCH>

R:Schaller, U.; Straub, C.; Kaempfer, U.; Rickli, E.E.

Protein Seq. Data Anal. 5, 21-25, 1992

A:Title: Complete amino acid sequence of ovine miniplasminogen.

A:Reference number: S28200; MUID:9314995; PMID:1492092

A:Accession: S28200

A:Molecule type: protein

A:Residues: 118-460 <SC2>

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z

F:1-37/Domain: activation peptide (fragment) #status experimental <APT>

F:38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>

F:41-118/Domain: kringle homology <KR4>

F:118-460/Product: miniplasminogen #status experimental <MIN>

F:132-211/Domain: kringle homology <KR5>

F:226-460/Domain: plasmin chain B #status experimental <BCH>

F:231-453/Domain: trypsin homology <TRY>

F:272,315,410/Active site: His, Asp, Ser #status predicted

Query Match 81.9%; Score 416; DB 2; Length 460;
Best Local Similarity 82.6%; Pred. No. 3.1e-37;
Matches 71; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 1 EODCMFNGKGYRGKATVTGTPCOEWAQEPHRSFTPGTNKWAQLEKNYCRNPDG 60
Db 129 EEDCMFNGKGYRGKATVTGTPCOEWAQEPHRSFTPGTNKWAQLEKNYCRNPDG 188

Qy 61 INGPWCYTNNPKRLFDYCDIPLCASS 86
Db 189 VGGPWCYTNNPKRLFDYCDIPLCASS 214

RESULT 5

A61545

plasmin (EC 3.4.21.7) precursor - horse (fragments)

N:Alternate names: plasminogen

N:Contains: miniplasminogen

C:Species: Equus caballus (domestic horse)

C:Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997

C:Accession: A61545; S17527

R:Schaller, U.; Rickli, E.E.

Enzyme 40, 63-69, 1988

A:Title: Structural aspects of the plasminogen of various species.

A:Reference number: A61545; MUID:8905015; PMID:3168975

A:Accession: A61545

A:Molecule type: protein

A:Residues: 1-33,34-117 <SCH>

R:Schaller, U.; Straub, C.; Kaempfer, U.; Rickli, E.E.

Protein Seq. Data Anal. 4, 69-74, 1991

A:Title: Complete amino acid sequence of equine miniplasminogen.

A:Reference number: S17527; MUID:92052077; PMID:1946332

A:Accession: S17527

A:Molecule type: protein

A:Residues: 118-455 <SC2>

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z

F:1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>

F:1-33/Domain: activation peptide (fragment) #status experimental <APT>

F:34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>

F:37-114/Domain: kringle homology <KR4>

F:118-455/Product: miniplasminogen #status experimental <MIN>

F:126-205/Domain: kringle homology <KR3>

F:126-455/Domain: plasmin chain B #status experimental <BCH>

F:226-448/Domain: trypsin homology <TRY>

F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 81.7%; Score 415; DB 2; Length 455;
Best Local Similarity 80.2%; Pred. No. 3.9e-37;
Matches 69; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EODCMFNGKGYRGKATVTGTPCOEWAQEPHRSFTPGTNKWAQLEKNYCRNPDG 60
Db 123 EEDCMFNGKGYRGKATVTGTPCOEWAQEPHRSFTPGTNKWAQLEKNYCRNPDG 182

Qy 61 INGPWCYTNNPKRLFDYCDIPLCASS 86
Db 183 VGGPWCYTNNPKRLFDYCDIPLCASS 208

RESULT 6

PLPG

plasmin (EC 3.4.21.7) precursor - pig (fragment)

N:Alternate names: plasminogen

N:Contains: miniplasminogen

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997

C:Accession: S03733; S03737; A25834

Rickli, J., Marti, T.; Roessellet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1,91-102, 1987
A>Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca
A:Reference number: 503733
A:Accession: 503733
R:Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNB fragments of human,
A:Reference number: 503735; PMID:81212097; PMID:7238497
A:Accession: 503737
A:Molecule type: protein
A:Residues: 1-57 <BRU>
R:Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A>Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A:Reference number: A25834; PMID:85203907; PMID:3846533
A:Accession: A25834
A:Molecule type: protein
A:Residues: 450-790 <MAR>
C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a var
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A:pathway: fibrinolysis
C:Keywords: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
F:1-790/Product: plasminogen-related protein predicted <PRO>
F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F:1-77/Domain: activation peptide #status predicted <APT>
F:78-560/Product: plasmin chain A #status predicted <ACH>
F:84-162/Domain: kringle homology <KR1>
F:166-243/Domain: kringle homology <KR2>
F:256-333/Domain: kringle homology <KR3>
F:358-435/Domain: kringle homology <KR4>
F:450-790/Product: miniplasminogen #status experimental <MIN>
F:461-560/Domain: kringle homology <KR5>
F:561-790/Product: plasmin chain B #status experimental <BGH>
F:561-793/Domain: trypsin homology <TRY>
F:30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,309
bonds: #status predicted
F:602,665,740/Active site: His, Asp, Ser #status predicted

Query Match 80.5%; Score 409; DB 1; Length 790;
Best local Similarity 80.0%; Pred. No. 3e-26;
Matches 68; Conservativity 5; Mismatches 12; Indels 0; Gaps 0;

OY 2 ODCMGKNGKVGRRKKATVTGTPCEWMAAOEPHRHSFIPTNKNALEKNYCNPQDI 61
DB 459 EDCCFGNGKRRGRGKRAITTVAGVPCQEWAADPEHRHSIFETPNRAELERNYCNPDGD 518
OY 62 NGPWCYTNNPRKLFDYCDIPLCASS 86
DB 519 NGPWCYTNNPQKLPDYCDVPQCCTS 543

RESULT 7
PLMS
plasmin (EC 3.4.21.7) precursor - mouse
N:Contains: angiotectatin; plasminogen
C:Species: Mus musculus (house mouse)
C>Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C:Accession: A38514; S48202; S48203
R:Degeen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A>Title: Characterization of the cDNA coding for mouse plasminogen and localization of t
A:Reference number: A38514; MUID:91184812; PMID:2081600
A:Accession: A38514
A:Molecule type: mRNA
A:Residues: 1-812 <DRG>
A:Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403
R:Jilka, H.R.; van Hoel, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 865-871, 1994

A>Title: Characterization of the murine plasma fibrinolytic system.
A:Reference number: S48202; MUID:95010076; PMID:7523120
A:Accession: S48202
A:Molecule type: protein
A:Residues: 20-25 <Lit>
A:Accession: S48203
A:Molecule type: protein
A:Residues: 22-27 <Lit>
C:Comment: plasminogen is synthesized by the kidney and is present in plasma and many other tissues. Plasminogen is converted into plasmin by plasminogen activators, both plasminogen mediators after dissociation from the clot. In the presence of the inhibitor, the activation is inhibited, the activation involves also removal of the activation peptide.
C:Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiotensin. Tissue plasminogen activator is a serine protease that converts plasminogen to plasmin.
C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of tissues; also activates the urokinase-type plasminogen activator.
A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolysis; plasminogen; plasminogen-related protein precursor homology <Lit>
F:1-96/Domain: plasminogen-related protein precursor homology <Lit>
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-812/Product: plasminogen #status predicted <PRO>
F:20-96/Domain: activation peptide #status predicted <AST>
F:79-466/Product: angiotensin #status predicted <AST>
F:97-581,582-812/Product: plasmin #status predicted <MAT>
F:97-581/Domain: chain A #status predicted <ACH>
F:103-181/Domain: kringle homology <KR1>
F:185-262/Domain: kringle homology <KR2>
F:275-352/Domain: kringle homology <KR3>
F:327-454/Domain: kringle homology <KR4>
F:481-560/Domain: kringle homology <KR5>
F:582-812/Domain: chain B #status predicted <BCH>
F:582-805/Domain: trypsin homology <TRY>
F:49-73, 53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,324-352/Domain: activation peptide #status predicted <AST>
F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
F:136,308/Binding site: carbonylate (Asn) (covalent) #status predicted
F:146-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
F:581-588/Cleavage site: Arg-Val (plasminogen activator) #status experimental
F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 79.9%; Score 406; DB 1; Length 812;
Best Local Similarity 79.1%; Pred. No. 6,5e-26;
Matches 68; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 1 BODCMFGNGKGRGKATVTGTPCOEMAAOEPRHSTFPTGNKMAGLEKNYCRNPDD 60
Db 478 ETDCTGNGKGRGKATVTGTPCOEMAAOEPRHSTFPTGNKMAGLEKNYCRNPDD 537

Qy 61 INGPWCYTMNPRKLPDYCDIPLCAS 86
Db 538 VNGPWCYTMNPRKLPDYCDIPLCAS 563

RESULT 8
PLBO
plasmin (BC 3.4.21.7) precursor - bovine
N:Alternate names: plasminogen
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1987 #sequence revision 28-Apr-1995 #text change 18-Jun-1999
A:Accession: S45046; A25835; I45961; S03736
R:Berghlund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A:Description: Cloning and characterization of the bovine plasminogen cDNA.
A:Reference number: S45046
A:Accession: S45046
A:Molecule type: mRNA
A:Residues: 1-812

A:Cross-references: EMBL:X79402; NID:g494962; PIDD:CAAS5939.1; PID:g494963
A:Experimental source: liver
A:Note: It is uncertain whether Met-1 or Met-8 is the initiator
R:Schaller, U.; Moser, P.W.; Danneberg-Muller, G.A.K.; Rossel, S.J.; Kamper, U.; Rick, R.

Eur. J. Biochem. 149, 267-278, 1985
 A/Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmin
 A/Reference number: A25835; MUID:85203906; PMID:3846532
 A/Accession: A25835
 A/Molecule type: protein
 A/Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
 R/Malinowski, D. P.; Sadler, J. E.; Davie, E. W.
 Biochemistry 23, 4243-4250, 1984
 A/Title: Characterization of a complementary deoxyribonucleic acid coding for human and
 A/Reference number: 145961; MUID:85023311; PMID:6148961
 A/Accession: 145961
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 706-743, 'R', 745-812 <MAL>
 A/Cross-references: GB:K02935; NID:g163551; PIDN:AAA0714.1; PID:g163552
 R/Brunsholz, R. A.; Letch, P. G.; Schaller, J.; Rickli, E. E.; Legerier, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1991
 A/Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
 A/Reference number: S03735; MUID:81212097; PMID:7238497
 A/Accession: S03735
 A/Molecule type: protein
 A/Residues: 27-83 <BRU>
 C/Function:
 A/Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 as the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A/Pathway: fibrinolysis
 C/Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
 C/Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringe; plasma;
 F/1-26/Domain: signal sequence #status predicted <SIG>
 F/8-103/Domain: plasminogen-related protein precursor homology <PLPH>
 F/27-812/Product: activation peptide #status experimental <PRO>
 F/27-103/Domain: activation peptide #status experimental <APR>
 F/104-583, 584-812/Product: plasmin #status experimental <MAT>
 F/104-583/Domain: plasmin chain A #status experimental <ACH>
 F/110-188/Domain: plasmin chain B #status experimental <KRI>
 F/192-269/Domain: kringe homology <KR2>
 F/282-359/Domain: kringe homology <KR3>
 F/384-461/Domain: kringe homology <KR4>
 F/485-564/Domain: kringe homology <KR5>
 F/584-812/Domain: plasmin chain B #status experimental <BCH>
 F/584-805/Domain: trypsin homology <TRY>
 F/56-80, 60-68, 110-188, 131-171, 159-183, 192-269, 195-323, 213-252, 241-264, 282-359, 303-342, 33
 bonds: #status predicted
 F/315/Binding site: carboxylate (Asn) (covalent) #status experimental
 F/365/Binding site: carboxylate (Ser) (covalent) #status experimental
 F/624, 667, 762/Active site: His, Asp, Ser #status predicted
 Query Match 79.9%; Score 406; DB 1; Length 812;
 Best Local Similarity 77.9%; Pred. No. 6, Se-36;
 Matches 67; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
 QY 1 EDDCMFNGKGYRGKATTTGTPCOEWAQEPHRSFTPGTNKAGLEKNYCRNDGD 60
 DB 482 EADCMIGTGKSYRGKATTAAGVPCQEWAAQEPHRSIFTPETNPOSGLEKNYCRNDGD 541
 QY 61 INGPWCYTNNPKRLFDYCDIPLCAS 86
 DB 542 VNGPWCTTNNPKRPFYCDVPCQESS 567

RESULT 9
 146260
 Plasmin (BC 3.4.21.7) precursor - western European hedgehog
 C/Species: Erinaceus europaeus (western European hedgehog)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C/Accession: 146260
 R/Jawn, R. M.; Boommark, N. W.; Schwartz, K.; Lindahl, G. E.; Wade, D. P.; Byrne, C. D.; Fong
 J. Biol. Chem. 270, 24004-24009, 1995
 A/Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot
 A/Reference number: 146259; MUID:96025778; PMID:7552597
 A/Accession: 146260
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA

A/Residues: 1-810 <LAW>
 A/Cross-references: EMBL:U33171; NID:g1046360; PID:g1046361
 C/Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology;
 C/Keywords: hydrolase; serine proteinase
 F/1-36/Domain: plasminogen-related protein precursor homology <PLPH>
 F/103-181/Domain: kringe homology <KRI>
 F/185-262/Domain: kringe homology <KR2>
 F/275-352/Domain: kringe homology <KR3>
 F/379-456/Domain: kringe homology <KR4>
 F/482-561/Domain: kringe homology <KR5>
 F/582-803/Domain: trypsin homology <TRY>
 Query Match 76.4%; Score 388; DB 2; Length 810;
 Best Local Similarity 77.6%; Pred. No. 5, Se-34;
 Matches 66; Conservative 3; Mismatches 16; Indels 0; Gaps 0;
 QY 1 EDDCMFNGKGYRGKATTTGTPCOEWAQEPHRSFTPGTNKAGLEKNYCRNDGD 60
 DB 479 EDDCIIDNGKGYRGVATTAAGTPCQAWAAQEPHRSIFTPETNPRADQENYCRNDGD 538
 QY 61 INGPWCYTNNPKRLFDYCDIPLCAS 85
 DB 539 ANGPWCYTNNPKRLFDYCDIPLCAS 563

RESULT 10
 A40522
 Plasmin (BC 3.4.21.7) precursor - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
 C/Accession: A40522
 R/Kanalaas, J. J.; Makker, S. P.
 J. Biol. Chem. 266, 10825-10829, 1991
 A/Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor s
 A/Reference number: A40522; MUID:9150378; PMID:1645711
 A/Accession: A40522
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-169 <VAN>
 A/Cross-references: GB:M62832; NID:G206215; PIDN:AAA1884.1; PID:9554488
 A/Note: the authors translated the codon TGT for residue 76 as Ala
 C/Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology;
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringe; serine proteinase
 F/24-112/Domain: kringe homology <KR2>
 F/24-112, 55-95, 83-107/Disulfide bonds: #status predicted
 Query Match 47.9%; Score 243.5; DB 2; Length 169;
 Best Local Similarity 48.2%; Pred. No. 4, Se-19;
 Matches 41; Conservative 12; Mismatches 31; Indels 1; Gaps 1;
 QY 2 QDCMFGNGKGYRGKATTTGTPCOEWAQEPHRSFTPGTNKAGLEKNYCRNDGD 61
 DB 32 QECYQNGKSYRGKATTTGTPCOEWAQEPHRSFTPGTNKAGLEKNYCRNDGD 90
 QY 62 NGPWCTTNNPKRLFDYCDIPLCAS 86
 DB 91 RGPWCFTTDPVSVMWEXCNKRCSET 115

RESULT 11
 JC5061
 macrophage-stimulating protein 1 precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
 C/Accession: JC5061
 R/Ohashiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamauchi, I.; Takaue, N.
 Biochem. Biophys. Res. Commun. 227, 273-280, 1996
 A/Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in t
 A/Reference number: JC5061; MUID:97011126; PMID:8858136
 A/Accession: JC5061
 A/Molecule type: mRNA
 A/Residues: 1-716 <OHS>
 A/Cross-references: EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; PID:g1669719

A;introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47
 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C;Superfamily: hepatocyte growth factor: kringle homology; trypsin homology
 C;Keywords: duplication; glycoprotein; growth factor; kringle
 F;1-31/Domain: signal sequence #status predicted <SIG>
 F;19-488-489-716/Product: macrophage-stimulating protein 1 #status experimental <MST>
 F;19-483/Domain: alpha chain #status experimental <ACH>
 F;110-186/Domain: kringle homology <KR1>
 F;191-268/Domain: kringle homology <KR2>
 F;292-370/Domain: kringle homology <KR3>
 F;379-457/Domain: kringle homology <KR4>
 F;484-711/Domain: beta chain #status experimental <BCH>
 F;489-709/Domain: trypsin homology <TRY>
 F;72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.1%; Score 239.5; DB 1; Length 716;

Best Local Similarity 48.8%; Pred. No. 5.6e-18; Mismatches 27; Indels 1; Gaps 1;

DB 377 ECGTSGSGEYKRGVSQKRGVOCQHWSSSTPHK-PQFTPSAPQAGLEAFGRNPDGDS 435

QY 62 NGPWCTYTNPRKLEFDYCDIPLC 83

DB 436 HGPWCYTLDPDILFDYCALQRC 457

RESULT 15

T18518

Apolipoprotein(a) - western European hedgehog (fragment)

C;Species: Erinaceus europaeus (western European hedgehog)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999

C;Accession: T18518

R;Lawn: R.M.; Boommarx, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong

J. Biol. Chem. 270, 24004-24009, 1995

A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein

A;Reference number: 146259; MUID:96025778; PMID:7592597

A;Accession: T18518

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-2869 <LAW>

A;Cross-references: EMBL:U33170; NID:G1046358; PID:G1046359; PIDN:AAC48522.1

A;Experimental source: liver

C;Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, contains apolipoprotein(a).

Query Match 47.0%; Score 239; DB 2; Length 2869;

Best Local Similarity 50.6%; Pred. No. 2.5e-17; Mismatches 31; Indels 2; Gaps 2;

DB 2589 EQLLENGENYQGNMAYISGQPCQGRKQTPRHHE-YTPENYPSKXLFQNYCRNPDGEI 2647

QY 62 NGPWCTYTNPRKLEFDYCDIPLCASS 86

DB 2648 -APWCYTTNSAVRMEYCSIFTCSS 2671

Search completed: January 12, 2004, 17:26:24
 Job time: 11.6391 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:17:22 : Search time 7.43609 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-10-088-548-8
Perfect score: 508
Sequence: 1 EDDCMFGNGKGYRGKATTV.....YTMNPKLFDYCDIPLCASS 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt 41.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	508	100.0	4548 1 APOA_HUMAN	P08519 homo sapien
2	432	85.0	810 1 PLMN_MACMU	P12545 macaca mula
3	430	84.6	810 1 PLMN_HUMAN	P00747 homo sapien
4	425	83.7	333 1 PLMN_CANFA	P80009 canis faml
5	416	81.9	343 1 PLMN_SHEEP	P81286 ovis aries
6	413	81.7	338 1 PLMN_HORSE	P80010 equus cabal
7	413	81.3	812 1 PLMN_MOUSE	P20918 mus musculu
8	409	80.5	790 1 PLMN_PIG	P06867 sus scrofa
9	406	79.9	812 1 PLMN_BOVIN	P06868 bos taurus
10	388	76.4	810 1 PLMN_BRIEU	Q29485 erinaceus e
11	243.5	47.9	169 1 PLMN_RAT	Q01177 rattus norv
12	241.5	47.5	711 1 HGFL_HUMAN	P26927 homo sapien
13	239.5	47.1	716 1 HGFL_MOUSE	P26928 mus musculu
14	236	46.5	1420 1 APOA_MACMU	P14417 macaca mula
15	234.5	46.2	728 1 HGF_HUMAN	P14210 homo sapien
16	227.5	44.8	728 1 HGF_MOUSE	Q08648 mus musculu
17	227.5	44.8	728 1 HGF_RAT	P17945 rattus norv
18	206.5	40.6	625 1 THRB_BOVIN	P00735 bos taurus
19	199.5	39.3	325 1 PLMN_PETMA	P33574 petromyzon
20	198.5	39.1	943 1 ROR2_HUMAN	Q01974 homo sapien
21	196.5	38.7	944 1 ROR2_MOUSE	Q92138 mus musculu
22	195	38.4	617 1 THRB_RAT	P18992 rattus norv
23	191.5	37.7	622 1 THRB_HUMAN	P00734 homo sapien
24	188.5	37.1	724 1 ROR2_DROME	Q9v6K3 drosophila
25	187	36.8	562 1 THRB_MOUSE	P00750 homo sapien
26	184	36.2	618 1 THRB_MOUSE	P19921 mus musculu
27	178.5	35.1	615 1 FAI2_HUMAN	P00748 homo sapien
28	170	33.5	566 1 TPA_BOVIN	Q28198 bos taurus
29	165.5	32.6	603 1 FAI2_CAVPO	Q04862 cavia porce
30	163.5	32.2	937 1 ROR1_HUMAN	Q02173 homo sapien
31	163.5	32.2	937 1 ROR1_MOUSE	Q92139 mus musculu
32	160	31.5	461 1 KRM2_MOUSE	Q98187 mus musculu
33	159.5	31.4	473 1 KRM1_MOUSE	Q99443 mus musculu

34	159.5	31.4	473 1 KRM1_RAT	Q92484 rattus norv
35	159	31.3	462 1 KRM2_HUMAN	Q9ncw0 homo sapien
36	159	31.3	559 1 TPA_MOUSE	P12114 mus musculu
37	156.5	30.8	475 1 KRM1_HUMAN	Q96m08 homo sapien
38	154.5	30.4	452 1 KRM1_XENLA	Q90y90 xenopus lae
39	154	30.3	559 1 TPA_RAT	P19637 rattus norv
40	154	30.3	655 1 HGFL_HUMAN	Q04756 homo sapien
41	146	28.7	442 1 UROK_PIG	P04185 sus scrofa
42	143	28.1	433 1 UROK_MOUSE	P06869 mus musculu
43	142	28.0	685 1 ROR1_DROME	Q24488 drosophila
44	139.5	27.5	593 1 FAI2_BOVIN	P98140 bos taurus
45	138	27.2	432 1 UROK_RAT	P29598 rattus norv

ALIGNMENTS

RESULT 1
APOA_HUMAN STANDARD; PRT; 4548 AA.
AC P08519;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
GN LpA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88039109; PubMed=3670400;
RA McLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
Plees G.W., Scanu A.M., Lawn R.M.;
RT "CDNA sequence of human apolipoprotein(a) is homologous to
RT plasminogen.";
RL Nature 330:132-137(1987).
RN [2]
RP SERINE PROTEASE ACTIVITY.
RX MEDLINE=90076123; PubMed=2531657;
RA Salonen E.-M., Jaahainen M., Zardi L., Vaheri A., Elmholt C.;
RT "Lipoprotein(a) binds to fibronectin and has serine proteinase
RT activity capable of cleaving it.";
RL EMBO J. 8:4035-4040(1989).
RN [3]
RP REVIEW.
RX MEDLINE=90049223; PubMed=2530631;
RA Utermann G.;
RT "The mysteries of lipoprotein(a).";
RL Science 246:904-910(1989).
RN [4]
RP CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
RX MEDLINE=21303595; PubMed=11294842;
RA Garner B., Merly A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
RT "Structural elucidation of the N- and O-glycans in conferring protease
RT apolipoprotein(a): role of O-glycans in conferring protease
RT resistance.";
RL J. Biol. Chem. 276:22200-22208(2001).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
RX MEDLINE=96217891; PubMed=8642595;
RA Mikol V., Lograsso P.V., Boettcher B.R.;
RT "Crystal structures of apolipoprotein(a) kringles IV37 free and
RT complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
RT acid: existence of novel and expected binding modes.";
RL J. Mol. Biol. 256:751-761(1996).
RN [6]
RP VARIANT ARG-4193.
RX MEDLINE=95002201; PubMed=7918682;
RA Scanu A.M., Pfaffinger D., Lee J.C., Himan J.;
RT "A single point mutation (Trp72-->Arg) in human apo(a) kringles 4-37
RT associated with a lysine binding defect in Lp(a)." ;

BL	Biochim Biophys Acta 1227:41-45(1994).
CC	- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
CC	(Lp(a)). It has serine proteinase activity and is able of
CC	auto proteolysis. Inhibits tissue-type plasminogen activator 1.
CC	Lp(a) may be a ligand for megalin/GP 330.
CC	- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
CC	decorin.
CC	- PTM: N- and O-glycosylated. The N-glycans are complex biantennary
CC	structures present in either a mono- or disialylated state. The
CC	O-glycans are mostly (80%) represented by the monosialylated core
CC	type I structure. NeuNAc6pa2-3Galbeta1-3GalNAc, with smaller
CC	amounts of disialylated and non-sialylated O-glycans also
CC	detected.
CC	- DISEASE: Elevated plasma concentrations of apo(a) and its
CC	naturally occurring proteolytic fragments are correlated with
CC	atherosclerosis. Homology with plasminogen kringle IV and V is
CC	thought to underlie the atherogenicity of the protein, because the
CC	MICELLANEOUS: Apo(a) is known to be proteolytically cleaved,
CC	leading to the formation of the so called mini-Lp(a). Apo(a)
CC	fragments accumulate in atherosclerotic lesions, where they may
CC	promote thrombogenesis. O-glycosylation may limit the extent of
CC	proteolytic fragmentation.
CC	- SIMILARITY: BELONGS TO PEPTIDASR FAMILY S1. PLASMINOGEN SUBFAMILY.
CC	- SIMILARITY: Contains 38 kringle domains.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
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CC	-----
DR	EMBL; X06290; CAA29618.1; .
DR	PIR; S00657; S00657
DR	PDB; 1I71; 1JUN-01.
DR	PDB; LUFN; 28-JUN-02.
DR	PDB; 1KIV; 18-MAY-99.
DR	PDB; 3KIV; 18-MAY-99.
DR	PDB; 4KIV; 18-MAY-99.
DR	MEROPS; S01.226; .
DR	Genew; HGNC:6667; LPA.
DR	MIM; 152200; .
DR	GO; GO:0004866; F:endopeptidase inhibitor activity; TAS.
DR	GO; GO:0008015; P:circulation; TAS.
DR	GO; GO:0009405; P:pachogonensis; TAS.
DR	InterPro; IPRO01314; Chymotrypsin.
DR	InterPro; IPRO00001; Kringle.
DR	InterPro; IPRO01254; Ser-protease_Try.
DR	pfam; PF000051; kringle; 38.
DR	pfam; PF000089; trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PRINTS; PR00018; KRINGLE.
DR	ProDom; PD000395; Kringle; 38.
DR	SMART; SM00130; KR; 38.
DR	SMART; SM00020; TRY_SPC; 1.
DR	PROSITE; PS00021; KRINGLE_1; 38.
DR	PROSITE; PS50070; KRINGLE_2; 38.
DR	PROSITE; PS50240; TRYPsin_DOM; 1.
DR	PROSITE; PS00134; TRYPsin_HIS; 1.
DR	PROSITE; PS00135; TRYPsin_SER; 1.
KW	Hydrolase; Serine protease; Lipid transport; Plasma; Glycoprotein;
KW	Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.
FT	SIGNAL 1 19
FT	CHAIN 20 4548
FT	DOMAIN 20 130
FT	DOMAIN 131 244
FT	DOMAIN 245 358
FT	DOMAIN 359 472
FT	DOMAIN 473 586
FT	DOMAIN 587 700
FT	DOMAIN 701 814
FT	DOMAIN 701 814
FT	APOLIPROTEIN(A).
FT	KRINGE TYPE IV, 1.
FT	KRINGE TYPE IV, 2.
FT	KRINGE TYPE IV, 3.
FT	KRINGE TYPE IV, 4.
FT	KRINGE TYPE IV, 5.
FT	KRINGE TYPE IV, 6.
FT	KRINGE TYPE IV, 7.

FT	DOMAIN	815	928	KRINGLE TYPE IV, 8.	
FT	DOMAIN	929	1042	KRINGLE TYPE IV, 9.	
FT	DOMAIN	1043	1156	KRINGLE TYPE IV, 10.	
FT	DOMAIN	1157	1270	KRINGLE TYPE IV, 11.	
FT	DOMAIN	1271	1384	KRINGLE TYPE IV, 12.	
FT	DOMAIN	1385	1498	KRINGLE TYPE IV, 13.	
FT	DOMAIN	1499	1612	KRINGLE TYPE IV, 14.	
FT	DOMAIN	1613	1726	KRINGLE TYPE IV, 15.	
FT	DOMAIN	1727	1840	KRINGLE TYPE IV, 16.	
FT	DOMAIN	1841	1954	KRINGLE TYPE IV, 17.	
FT	DOMAIN	1955	2068	KRINGLE TYPE IV, 18.	
FT	DOMAIN	2069	2182	KRINGLE TYPE IV, 19.	
FT	DOMAIN	2183	2296	KRINGLE TYPE IV, 20.	
FT	DOMAIN	2297	2410	KRINGLE TYPE IV, 21.	
FT	DOMAIN	2411	2524	KRINGLE TYPE IV, 22.	
FT	DOMAIN	2525	2638	KRINGLE TYPE IV, 23.	
FT	DOMAIN	2639	2752	KRINGLE TYPE IV, 24.	
FT	DOMAIN	2753	2866	KRINGLE TYPE IV, 25.	
FT	DOMAIN	2867	2980	KRINGLE TYPE IV, 26.	
FT	DOMAIN	2981	3094	KRINGLE TYPE IV, 27.	
FT	DOMAIN	3095	3208	KRINGLE TYPE IV, 28.	
FT	DOMAIN	3209	3322	KRINGLE TYPE IV, 29.	
FT	DOMAIN	3323	3436	KRINGLE TYPE IV, 30.	
FT	DOMAIN	3437	3550	KRINGLE TYPE IV, 31.	
FT	DOMAIN	3551	3664	KRINGLE TYPE IV, 32.	
FT	DOMAIN	3665	3770	KRINGLE TYPE IV, 33.	
FT	DOMAIN	3771	3884	KRINGLE TYPE IV, 34.	
FT	DOMAIN	3885	3998	KRINGLE TYPE IV, 35.	
FT	DOMAIN	3999	4112	KRINGLE TYPE IV, 36.	
FT	DOMAIN	4113	4226	KRINGLE TYPE IV, 37.	
FT	DOMAIN	4227	4327	KRINGLE TYPE V.	
FT	DOMAIN	4328	4548	SERINE PROTEASE.	
FT	ACT_SITE	4369	4369	CHARGE RELAY SYSTEM.	
FT	ACT_SITE	4412	4412	CHARGE RELAY SYSTEM.	
FT	ACT_SITE	4498	4498	CHARGE RELAY SYSTEM.	
FT	VARIANT	4193	4193	W -> R (LOSS OF LYSINE-SEPHAROSE BINDING).	
FT	SEQUENCE	4548 AA;	501313 MM;	/FTID=VAR_006633.	
FT	SEQ			96521B596A465C5F CRC64;	
Query Match					
Best Local Similarity 100.0%; Score 508; DB 1; Length 4548;					
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	EODCMFENGNGKYGKKA	TTTTGTCTGCQMAQEPHRASTFI	PGTKMKAGLEKNYGRNP	PGD 60
DB	4225	EODCMFENGNGKYGKKA	TTTTGTCTGCQMAQEPHRASTFI	PGTKMKAGLEKNYGRNP	PGD 4284
QY	61	INGPWCYTNP	PRKLF	FDYCDIPL	CLASS 86
DB	4285	INGPWCYTNP	PRKLF	FDYCDIPL	CLASS 4310

RL J. Biol. Chem. 264:5957-5965(1989).

CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
 CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.

CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.

CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTITRYPASIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
 CC INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD
 CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.

CC -1- SIMILARITY: Contains 5 kringle domains.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sib-sib.ch).

CC -----
 CC EMBL: J04697; AAA36901.1; -
 CC PIR: B32869; B30848.
 CC HSSP: P00747; 1PMK.

DR MEROPS: S01.233; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser protease_Try.
 DR Pfam: PF00051; kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 5.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRY_SPC; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Plasmin; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.

FT SIGNAL 1 19
 FT CHAIN 20 810 PLASMINOGEN.
 FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
 FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 181 103 KRINGLE 1.
 FT DOMAIN 184 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 377 454 KRINGLE 4.
 FT DOMAIN 481 560 KRINGLE 5.
 FT DOMAIN 581 810 SERINE PROTEASE.
 FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.

FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
 FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
 FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 158 158 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 432 432 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 134 134 FIBRIN.
 FT BINDING 136 136 FIBRIN.
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 185 262 BY SIMILARITY.
 FT DISULFID 188 316 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 352 BY SIMILARITY.
 FT DISULFID 296 335 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 567 685 BY SIMILARITY.
 FT DISULFID 577 623 BY SIMILARITY.
 FT DISULFID 607 766 BY SIMILARITY.
 FT DISULFID 699 745 BY SIMILARITY.
 FT DISULFID 729 784 BY SIMILARITY.
 FT DISULFID 756 784 BY SIMILARITY.
 FT CARBOHYD 365 365 O-LINKED (GLYNAAC...) (BY SIMILARITY).
 SQ SEQUENCE 810 AA; 90255 MW; A/5E1CS1A1A0F24A C6C64;

Query Match 85.0%; Score 432; DB 1; Length 810;
 Best Local Similarity 83.7%; Pred. No. 1.6e-40;
 Matches 72; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTTGTGCEWAAQEPHRSFFIFGTNKALEKNYCNPDGD 60
 DB 478 EDDCMFGNGKGYRGKATTTGTGCEWAAQEPHRSIFETBETNPRAGLEKNYCNPDGD 537

QY 61 INGPWCYTMNPRKLPDYCDIPLCLASS 86
 DB 538 VGGPWCYTMNPRKLPDYCDVPCAS 563

RESULT 3
 PLNM HUMAN STANDARD; PRT; 810 AA.
 ID PLNM HUMAN
 AC P00747;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
 GN PLG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9020879; PubMed=2318848;
 RA Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;
 RT "Characterization of the gene for human plasminogen, a key proenzyme
 RT in the fibrinolytic system";
 RL J. Biol. Chem. 265:6104-6111(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87162490; PubMed=3030813;
 RA Foregren M., Raden B., Israelsson M., Larsson K., Heden L.-O.;

RT "Molecular cloning and characterization of a full-length cDNA clone
RT for human plasminogen.";
RL FEBS Lett. 213:254-260(1987).
RN (13)
RP SEQUENCE OF 20-810.
RA Sottrup-Jensen L., Petersen T.E., Magnusson S.;
RL Submitted (JUL-1977) to the PIR data bank.
RN (14)
RP SEQUENCE OF 292-810 FROM N.A.
RX MEDLINE=85023311; PubMed=6149961;
RA Malinowski D.P., Sadler J.E., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT human and bovine plasminogen.";
RL Biochemistry 23:4243-4250(1984).
RN (15)
RP SEQUENCE OF 20-100.
RX MEDLINE=75093329; PubMed=122932;
RA Wiman B., Wallen P.;
RT "Structural relationship between 'glutamic acid' and 'lysine' forms
RT of human plasminogen and their interaction with the NH2-terminal
RT activation peptide as studied by affinity chromatography.";
RL Eur. J. Biochem. 50:489-494(1975).
RN (16)
RP SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810.
RA Sottrup-Jensen L., Claeys H., Zajdel M., Petersen T.E., Magnusson S.;
RL (In) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);
RT Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
RL Raven Press, New York (1978).
RN (17)
RP SEQUENCE OF 483-604.
RX MEDLINE=76043692; PubMed=126863;
RA Wiman B., Wallen P.;
RT "Amino-acid sequence of the cyanogen-bromide fragment from human
RT plasminogen that forms the linkage between the plasmin chains.";
RL Eur. J. Biochem. 58:539-547(1975).
RN (18)
RP SEQUENCE OF 581-810.
RX MEDLINE=77225245; PubMed=142009;
RA Wiman B.;
RT "Primary structure of the B-chain of human plasmin.";
RL Eur. J. Biochem. 76:129-137(1977).
RN (19)
RP ACTIVE SITE.
RX MEDLINE=73149248; PubMed=4694729;
RA Robbins K.C., Bernabe P., Arradon L., Summaria L.;
RT "The primary structure of human plasminogen. II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence.";
RL J. Biol. Chem. 248:1631-1633(1973).
RN (10)
RP ACTIVE SITE.
RX MEDLINE=69234739; PubMed=4240117;
RA Grothkopf W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue.";
RL J. Biol. Chem. 244:3590-3597(1969).
RN (11)
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE=82213905; PubMed=6919539;
RA Texter M., Valli Z., Patchy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringle 4.";
RL J. Biol. Chem. 257:7401-7406(1982).
RN (12)
RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE=85054794; PubMed=6094526;
RA Valli Z., Patchy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringle 1 domain.";
RL J. Biol. Chem. 259:13690-13694(1984).
RN (13)
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE=97345939; PubMed=9201958;

RA Wang H., Prorok M., Bretthauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen.";
RL Biochemistry 36:8100-8106(1997).
RN (14)
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
RN (15)
RP CARBOHYDRATE-LINKAGE SITE SER-268.
RX MEDLINE=97207306; PubMed=9054441;
RA Pirte-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RA Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
RT human plasminogen 2.";
RL J. Biol. Chem. 272:7408-7411(1997).
RN (16)
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
RL Cell 79:315-328(1994).
RN (17)
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=97238710; PubMed=9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
RA Lapevich R., Nacy C.A.;
RT "A recombinant human angiostatin protein inhibits experimental primary
RT and metastatic cancer.";
RL Cancer Res. 57:1329-1334(1997).
RN (18)
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=92031502; PubMed=1657148;
RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
RT refined at 1.9-A resolution.";
RL Biochemistry 30:10576-10588(1991).
RN (19)
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=92031503; PubMed=1657149;
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringle 4.";
RL Biochemistry 30:10589-10594(1991).
RN (20)
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RX Sec B., Yamano A., Whitlow M., Teeter M.W.;
RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
RT A possible structural role of disordered residues.";
RL Acta Crystallogr. D 53:169-178(1997).
RN (21)
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE=96180691; PubMed=8611560;
RA Mathews I.I., Vanderhoff-Hanover P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringle 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid.";
RL Biochemistry 35:2567-2576(1996).
RN (22)
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE=98198034; PubMed=9521645;
RA Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringle
RT 5 domain of human plasminogen.";
RL Biochemistry 37:3258-3271(1998).

RN [23]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237157; PubMed=8181475;
 RA Rejante M.R., Llinas M.,
 RT "1H-NMR assignments and secondary structure of human plasminogen
 kringles 1.";
 RL Eur. J. Biochem. 221:927-937(1994).
 RN [24]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237158; PubMed=8181476;
 RA Rejante M.R., Llinas M.,
 RT "Solution structure of the epsilon-aminohexanoic acid complex of
 human plasminogen kringles 1.";
 RL Eur. J. Biochem. 221:939-949(1994).
 RN [25]
 RP STRUCTURE BY NMR OF 183-354.
 RX MEDLINE=96194156; PubMed=8652577;
 RA Soehndel S., Hu C.-K., Marti D., Afolter M., Schaller J., Llinas M.,
 RA Rickli B.E.,
 RT "Recombinant gene expression and 1H NMR characteristics of the
 kringles (2 + 3) supermodule: spectroscopic/functional individuality
 of plasminogen kringles domains.";
 RL Biochemistry 35:2357-2364(1996).
 RN [26]
 RP STRUCTURE BY NMR OF 374-461.
 RX MEDLINE=90219023; PubMed=2157850;
 RA Atkinson R.A., Williams R.J.P.,
 RT "Solution structure of the kringles 4 domain from human plasminogen by
 1H nuclear magnetic resonance spectroscopy and distance geometry.";
 RL J. Mol. Biol. 212:541-552(1990).
 RN [27]
 RP VARIANTS PHE-374 AND THR-620.

Query Match 84.6%; Score 430; DB 1; Length 810;
 Best Local Similarity 82.4%; Pred. No. 2.7e-40;
 Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGYRGKATTTGTPCOEWAQBPFRHSFTPGTNKAGLEKNCRNPDGD 60
 DB 478 EDDCMFGNGYRGKATTTGTPCOEWAQBPFRHSFTPGTNKAGLEKNCRNPDGD 537
 QY 61 INGPWCYTANPRKLPDYCDIPLCAS 85
 DB 538 VGSPWCYTANPRKLPDYCDIPLCAS 562

RESULT 4
 PLMN CANFA STANDARD; PRT; 333 AA.
 AC P80009;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN PLG.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI TaxID=9615;
 RN [1]_TaxID=9615;
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=90175323; PubMed=2626424;
 RA Schaller J., Straub C., Kaempfer U., Rickli B.E.,
 RT "Complete amino acid sequence of canine miniplasminogen.";
 RL Protein Seq. Data Anal. 2:445-450(1989).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,

CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. ACTIVATED WITH UROKINASE AND HIGH CONCENTRATIONS OF
 CC STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains at least 1 kringles domain.
 DR HSSP; P00747; SHPG.
 DR MEROPS; S01.233; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringles.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00051; kringles; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringles; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringles; Zymogen.
 KM NON_TER 1
 FT CHAIN 1
 FT CHAIN 104 103
 FT DOMAIN 4 83
 FT DOMAIN 104 333
 FT DISULFID 4 83
 FT DISULFID 25 66
 FT DISULFID 54 78
 FT DISULFID 90 208
 FT DISULFID 100 108
 FT DISULFID 130 146
 FT DISULFID 222 289
 FT DISULFID 252 268
 FT DISULFID 279 307
 FT ACT_SITE 145 145
 FT ACT_SITE 188 188
 FT ACT_SITE 283 283
 FT SITE 152 152
 FT SITE 186 186
 FT SITE 264 264
 FT SITE 277 277
 SQ SEQUENCE 333 AA; 36678 MW; C8C0271B6C6A8D4 CRC64;

Query Match 83.7%; Score 425; DB 1; Length 333;
 Best Local Similarity 84.5%; Pred. No. 3.8e-40;
 Matches 71; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 QY 3 DCMFGNGYRGKATTTGTPCOEWAQBPFRHSFTPGTNKAGLEKNCRNPDGD 62
 DB 3 DCMFGNGYRGKATTTGTPCOEWAQBPFRHSFTPGTNKAGLEKNCRNPDGD 62
 QY 63 GPCWCYTANPRKLPDYCDIPLCAS 86
 DB 63 GPCWCYTANPRKLPDYCDIPLCAS 86
 RESULT 5
 PLMN SHEEP STANDARD; PRT; 343 AA.

AC	P81286; 1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Plasminogen (EC 3.4.21.7) (Fragment).
GN	PLG.
OS	Ovis aries (sheep).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Caprinae; Ovis.
OX	NCB1_taxid=9940;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=9314995; PubMed=1492092;
RA	Schaller J., Straub C., Kampfer U., Rickli E.E.;
RT	"Complete amino acid sequence of ovine multiplasminogen."
RL	Protein Seq. Data Anal. 5:21-25(1992).
CC	-1 FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION. IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UKROINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMBANTIC AND VON WILLEBRAND FACTOR.
CC	-1 CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.
CC	-1 ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STEPTOKINASE.
CC	-1 MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC	-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY. -1 SIMILARITY: Contains at least 2 kringle domains.
CC	PIR; B61545; B61545.
DR	HSSP; P00747; SHPG.
DR	MEROPS; S01.233; -.
DR	InterPro; IPR001314; Chymotrypsin.
DR	InterPro; IPR000001; Kringle.
DR	InterPro; IPR003966; Prothrombin.
DR	InterPro; IPR01254; Ser-protease_Try.
DR	pIam; PF00051; Kringle_1.
DR	pIam; PF00089; tryptase; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PRINTS; PR00018; KRINGLE.
DR	PRINTS; PR01505; PROTHROMBIN.
DR	Prodont; PD00395; Kringle; 1.
DR	SMART; SMO0130; KR; 1.
DR	SMART; SMO0020; Tryp_Spc; 1.
DR	PROSITE; PS00021; KRINGLE_1; 1.
DR	PROSITE; PS00070; KRINGLE_2; 1.
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW	Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
FT	NON_TER 1 1
FT	DOMAIN <1 140 HEAVY CHAIN A.
FT	DOMAIN 141 >343 LIGHT CHAIN A.
FT	DOMAIN <1 17 KRINGLE 4.
FT	DOMAIN 41 120 KRINGLE 5.
FT	DOMAIN 114 341 SERINE PROTEASE.
FT	ACT_SITE 181 181 CHARGE RELAY SYSTEM.
FT	ACT_SITE 224 224 CHARGE RELAY SYSTEM.
FT	ACT_SITE 319 319 CHARGE RELAY SYSTEM.
FT	NON_TER 343 343
SO	SEQUENCE 343 AA; 37662 MW; 8DF6EBA92D596EE0 CRC64;
Query Match	81.9%; Score 416; DB 1; Length 343;
Best Local Similarity	82.6%; Pred. NO. 4e-39; 14; Indels 0; Gaps 0;
Matches 71; Conservative	1; Mismatches 0; Indels 0; Gaps 0;

QY	1	EOOCMBNGGVGKATATVTCGCEMAAOEHRHSTFIPGNWKAIGLKKYCNRPDD	6
DB	12	EADDMGLGIGGVGKATVAVGPCEMAQEPHRHGIFTPETNPRAGLEKYNCRNPDD	71
QY	61	INGFWCYTNPRKLPDYCDIPLCASS 86	
DB	72	VNGPWCTTNPRLFDYCDIPQCESS 97	
RESULT 6			
PLAN	HORSE	STANDARD;	PRT; 338 AA.
ID	PLANK HORSE		
AC	P80010;		
DT	01-NOV-1991 (Rel. 20, Created)		
DT	01-NOV-1991 (Rel. 20, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Plasminogen (EC 3.4.21.7) (Fragment).		
GN	PLG.		
OS	Equus caballus (Horse).		
OC	Bufoarctia, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
OX	NCBI_TaxID=9796;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Plasma;		
RA	MEDLINE=92052077; PubMed=1946332;		
RA	Schaller J., Straub C., Kaempfer U., Rickli B.E.;		
RT	"Complete amino acid sequence of equine miniplasminogen."		
RL	Protein Seq. Data Anal. 4:69-74(1991).		
CC	-1- FUNCTION. PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING		
CC	EMBRIONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION		
CC	AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE		
CC	GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN		
CC	ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH		
CC	AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,		
CC	LAMININ AND VON WILLEBRAND FACTOR.		
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Lys- -Xaa > Arg- -Xaa;		
CC	higher selectivity than trypsin. Converts fibrin into soluble		
CC	products.		
CC	-1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN		
CC	ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO		
CC	FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STEPTOKINASE.		
CC	-1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN		
CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.		
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.		
CC	-1- SIMILARITY: Contains at least 1 kringle domain.		
CC	PIR: A61545; A61545.		
DR	HSSP; P00747; SHRP.		
DR	MEROPE; S01.233; -.		
DR	InterPro: IPR001314; Chymotrypsin.		
DR	InterPro: IPR000001; Kringle.		
DR	InterPro: IPR003966; Prothrombin.		
DR	InterPro: IPR001254; Ser protease_Try.		
DR	Pfam; PF00051; kringle; 1.		
DR	Pfam; PF00089; trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	PRINTS; PR00018; KRINGLE.		
DR	PRINTS; PR01505; PROTHROMBIN.		
DR	ProDom; PD000395; Kringle; 1.		
DR	SMART; SM00130; KR; 1.		
DR	SMART; SM00020; TRY_P_SPC; 1.		
DR	PROSITE; PS00021; KRINGLE_1; 1.		
DR	PROSITE; PS00070; KRINGLE_2; 1.		
DR	PROSITE; PS02040; TRYPSIN_DOM; 1.		
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.		
DR	PROSITE; PS00135; TRYPSIN_SER; 1.		
KW	Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;		
KW	Tissue remodeling; Blood coagulation; Kringle; Zymogen.		
FT	NON TER	1	
FT	CHAIN	<1	108 PLASMIN HEAVY CHAIN A.
FT	CHAIN	109	338 PLASMIN LIGHT CHAIN B.
FT	DOMAIN	9	88 KRINGLE 5.

DR InterPro: IPR000001; Kringle-
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan. app.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser. protease. try.
 DR Pfam: PF00051; Kringle. 5.
 DR Pfam: PF00024; PAN. 1.
 DR Pfam: PF00089; trypsin. 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0018; KRINGLE.
 DR PRINTS: PRO1505; PROTHROMBIN.
 DR PRODOM: PD000395; Kringle. 5.
 DR SMART: SM00130; KR. 5.
 DR SMART: SM00473; PAN AP. 1.
 DR SMART: SM00020; TRY. SPC. 1.
 DR PROSITE: PS00021; KRINGLE. 1; 5.
 DR PROSITE: PS50070; KRINGLE. 2; 5.
 DR PROSITE: PS50240; TRYPSIN DOM. 1.
 DR PROSITE: PS00134; TRYPSIN HIS. 1.
 DR PROSITE: PS00135; TRYPSIN SER. 1.
 KW Hydroxylase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.
 FT CHAIN 1 19 PLASMINOGEN.
 FT CHAIN 20 812 PLASMIN HEAVY CHAIN A.
 FT CHAIN 20 581 ACTIVATION PEPTIDE.
 FT PEPTIDE 20 97 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 98 581 ANGIOSTATIN.
 FT CHAIN 98 7436 PLASMIN LIGHT CHAIN B.
 FT CHAIN 582 812 KRINGLE 1.
 FT DOMAIN 103 181 KRINGLE 2.
 FT DOMAIN 184 262 KRINGLE 3.
 FT DOMAIN 275 352 KRINGLE 4.
 FT DOMAIN 377 454 KRINGLE 5.
 FT DOMAIN 481 560 KRINGLE 6.
 FT DOMAIN 582 812 SERINE PROTEASE.
 FT ACT SITE 624 624 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 667 667 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 185 262 BY SIMILARITY.
 FT DISULFID 188 316 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 352 BY SIMILARITY.
 FT DISULFID 296 335 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 568 687 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 578 586 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 609 625 BY SIMILARITY.
 FT DISULFID 701 768 BY SIMILARITY.
 FT DISULFID 731 747 BY SIMILARITY.
 FT DISULFID 758 786 BY SIMILARITY.
 FT CONFLICT 235 235 R -> H (IN REF. 1).
 FT CONFLICT 525 525 G -> D (IN REF. 1).
 FT CONFLICT 649 649 S -> L (IN REF. 1).
 SQ SEQUENCE 812 AA; 90781 MW; 241732606A2FFD2 CRC64;

Query Match 81.3%; Score 413; DB 1; Length 812;
 Best Local Similarity 80.2%; Pred. No. 2.1e-38;
 Matches 69; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
 1 EDCMFGNGKGYGKATVGTGFCQEWAAQEPHHSITPNTKMAGLEKNCYCRNPDGD 60

DB 478 ETDGWTGNGKDYRGKATVTAAGTFCQGWAAQEPHHSITPNTNPRAGLEKNCYCRNPDGD 537
 QY 61 INGPWCYTNNPRKLPDYCDIPLCASS 86
 DB 538 VNGPWCYTNNPRKLPDYCDIPLCASS 563
 RESULT 8
 PLAN_PIG
 ID PLAN_PIG STANDARD; PRT; 790 AA.
 AC P06867;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen (EC 3.4.21.7).
 GN PLG.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE OF 1-560.
 RA Schaller J., Marti T., Roeseleat S.J., Kaempfer U., Rickli E.E.;
 RT "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
 of the carbohydrate attachment sites with the human and bovine
 species.";
 RL Fibrinolysis 1:91-102(1987).
 RN [2]
 RP SEQUENCE OF 450-790.
 RX MEDLINE=85203907; Pubmed=3846533;
 RA Marti T., Schaller J., Rickli E.E.;
 RT "Determination of the complete amino-acid sequence of porcine
 miniplasminogen.";
 RL Eur. J. Biochem. 149:279-285(1985).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; Pubmed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 plasminogen. Species specificity in relation to stalylation and
 fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa;
 higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCAN CONTAINS N-ACETYLACTOSAMINE, SIALIC ACID AND
 IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAc
 DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
 (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 DR HSSP: P00747; SHPG.
 DR MEROPS: S01.233; -.
 DR GlycosultedB: P06867; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.

DR InterPro: IPR003609; Pan app.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00051; Kringle_5.
DR Pfam: PF00024; PAN_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR ProDom: PD000395; Kringle_5.
DR SMART: SM00130; KR_5.
DR SMART: SM00473; PAN_AP_1.
DR SMART: SM00020; Tryp_Spc_1.
DR PROSITE: PS00021; KRINGLE_2_5.
DR PROSITE: PS00707; KRINGLE_2_5.
DR PROSITE: PS01040; TRYPsin_DOM_1.
DR PROSITE: PS00134; TRYPsin_HIS.
DR PROSITE: PS00135; TRYPsin_SER_1.
DR KEGG: Hydroxylase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KM Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
FT CHAIN 1 560 PLASMIN HEAVY CHAIN A.
FT CHAIN 561 790 SERINE PROTEASE.
FT DOMAIN 561 790 KRINGLE 1.
FT DOMAIN 84 162 KRINGLE 2.
FT DOMAIN 166 243 KRINGLE 3.
FT DOMAIN 256 333 KRINGLE 4.
FT DOMAIN 358 435 KRINGLE 5.
FT DOMAIN 461 540 CHARGE RELAY SYSTEM.
FT ACT_SITE 602 602 CHARGE RELAY SYSTEM.
FT ACT_SITE 645 645 CHARGE RELAY SYSTEM.
FT ACT_SITE 740 740 CHARGE RELAY SYSTEM.
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 340 340 /FTID=CAR_000019.
FT CARBOHYD 340 340 O-LINKED (GALNAC. . .).
FT CARBOHYD 340 340 /FTID=CAR_000020.
SQ SEQUENCE 790 AA; 88592 MW; F04EA06E74BCD58E CRC64;

Query Match 80.5%; Score 409; DB 1; Length 790;
Best Local Similarity 80.0%; Pred. No. 5.7e-38;
Matches 68; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 2 ODCMFGNGKGVGRKATVTGTPCOEMAQOBPHRSTIPGNNKAGLEKQYCRNPDDGI 61
DB 459 EDCMFGNGKGVGRKATVTGTPCOEMAQOBPHRSTIPGNNKAGLEKQYCRNPDDGI 518
QY 62 NGPWCYTNAPRKLFDYCDIPLCASS 86
DB 519 NGPWCYTNAPRKLFDYCDIPLCASS 543

RESULT 9
PLMN_BOVIN STANDARD; PRT; 812 AA.
ID AC P06868; Q28162; DT 01-JAN-1988 (Rel. 06, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update) DE Plasmalogen precursor (EC 3.4.21.7). GN PLC. OS Bos taurus (Bovine). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. OX NCBI_TaxID=9913; RN 11
RP SEQUENCE FROM N.A. RC TISSUE=Liver; RA Berglund L., Andersen M.D., Petersen T.E.; RT "Cloning and characterization of the bovine plasminogen cDNA."; RL Int. Dairy J. 5:593-603(1995).
RX MEDLINE=85203906; PubMed=3846532;

RA Schaller J., Moser P.W., Danneberg-Muller G.A.K., Rosselet S.J.,
RA Kampfer U., Rickli E.B.;
RT "Complete amino acid sequence of bovine plasminogen. Comparison with
RT human plasminogen.";
RL Eur. J. Biochem. 149:267-278(1985).
RN [3]
RP SEQUENCE OF 706-812 FROM N.A.
RX MEDLINE=85023311; PubMed=6148961;
RA Maitinowski D.P., Sadler J.E., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT human and bovine plasminogen.";
RL Biochemistry 23:4243-4250(1984).
RN [4]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Matti T., Schaller J., Rickli E.B., Schmid K., Kamberling J.P.,
RA Gerwig G.J., van Halbeek H., Vilegenthart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRANULOSA FOLLICLE. IT ACTIVATES THE UKONINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOCENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- PTM: N-LINKED GLYCANS CONTAIN N-ACETYLACTOSAMINE AND SIALIC ACID.
CC O-LINKED GLYCANS CONSIST OF GAL-GALNAC DISACCHARIDE WITH IS
CC MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-gib.ch).
CC
CC EMBL; X79402; CAA55939.1; -
DR EMBL; K02935; AAA30714.1; -
DR HSP, S45046; PLEB.
DR HSP, P00747; 2PK4.
DR MEROPS; S01.233; -
DR GlycoSiteDB; P06868; -
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; Kringle_5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle_5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; TRYF_Spc; 1.

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DR PROSITE; PS00021; KRINGLE 1; 5.
DR PROSITE; PS00070; KRINGLE 2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KM Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL. 1 26
FT CHAIN 27 812 PLASMINOGEN.
FT CHAIN 27 583 PLASMIN HEAVY CHAIN A.
FT CHAIN 584 812 PLASMIN LIGHT CHAIN B.
FT DOMAIN 110 188 KRINGLE 1.
FT DOMAIN 192 269 KRINGLE 2.
FT DOMAIN 282 359 KRINGLE 3.
FT DOMAIN 384 461 KRINGLE 4.
FT DOMAIN 485 564 KRINGLE 5.
FT DOMAIN 584 812 SERINE PROTEASE.
FT DOMAIN 315 315 N-LINKED (GLCNAC. . .).
FT CARBOHYD /FTID-CAR 000014.
FT CARBOHYD 315 315 O-LINKED TGNAC. . .).
FT CARBOHYD 365 365 /FTID-CAR 000015.
FT ACT SITE 624 624 CHARGE RELAY SYSTEM.
FT ACT SITE 667 667 CHARGE RELAY SYSTEM.
FT ACT SITE 762 762 CHARGE RELAY SYSTEM.
FT CONFLICT 335 335 N -> D (IN REF. 2).
FT CONFLICT 516 516 O -> H (IN REF. 2).
FT CONFLICT 555 555 P -> L (IN REF. 2).
FT CONFLICT 744 744 T -> R (IN REF. 3).
FT SEQUENCE 812 AA; 91216 MW; 38A6AA691E220946 CRC64;

Query Match 79.9%; Score 406; DB 1; Length 812;
Best Local Similarity 77.9%; Pred. No. 1,3e-37;
Matches 67; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 1 EODCMGNGKGYRGKATVTGTPCEMAAQBHRHSTFPGTNKWAAGLEKNTCRNPDDG 60
Db 482 EADCMIGTGKSYRGKATVTAGVPCQMAAQBHRHSTFPGTNKWAAGLEKNTCRNPDDG 541
Qy 61 INGPWCYTNNPRKLPDYCDPLFCASS 86
Db 542 VNGPWCYTNNPRKLPDYCDVPCASS 567

RESULT 10
PLAN_ENTRY STANDARD; PRT; 810 AA.
AC Q29485;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen precursor (BC 3.4.21.7).
GN PLG.
OS Etrineaus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=96025778; PubMed=7592597;
RA Lawn R.M., Boomark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
RA Byrne C.D., Pong K.J., Meer K., Patchy L.;
RT "The recurring evolution of lipoprotein(a). Insights from cloning of
RT hedgehog apolipoprotein(a).";
RT J. Biol. Chem. 270:24004-24009 (1995).
RN [2]
RP REVISIONS.
RA Lawn R.M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,

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CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE
CC -!- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC -!- IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -!- SIMILARITY: Contains 5 kringle domains.
CC -----
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CC -----
DR EMBL; U3171; AAC48717.1; -.
DR PIR; I46260; I46260.
DR HSSP; P00747; 1PMK.
DR MEROPS; S01.233; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003609; Pan. app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00021; KRINGLE 1; 5.
DR PROSITE; PS00070; KRINGLE 2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
FT DOMAIN 103 181 SERINE PROTEASE.
FT DOMAIN 185 262 KRINGLE 1.
FT DOMAIN 275 352 KRINGLE 2.
FT DOMAIN 379 456 KRINGLE 3.
FT DOMAIN 482 561 KRINGLE 4.
FT DOMAIN 582 622 KRINGLE 5.
FT ACT SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT SITE 665 665 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT CARBOHYD 339 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 810 AA; 90902 MW; 8E75780946017A16 CRC64;

Query Match 76.4%; Score 388; DB 1; Length 810;
Best Local Similarity 77.6%; Pred. No. 1,3e-35;
Matches 66; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EODCMGNGKGYRGKATVTGTPCEMAAQBHRHSTFPGTNKWAAGLEKNTCRNPDDG 60

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DB 479 EDCIIDNGKGYGTATTCAGTCACMAAOBPHRHSIFPETNPADLOENYCRNPDGD 538
QY 61 INGPWCYTMNPRKLPYCDIPLCAS 85
DB 539 ANGPWCYTMNPRKLPYCDIPHCVS 563

RESULT 11
PLNM RAT STANDARD; PRT; 169 AA.
ID 001177;
AC 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN P1G.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanakas J.U., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen.";
RL J. Biol. Chem. 266:10825-10829(1991).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa]-Arg-[Xaa];
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC -----
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CC -----
DR EMBL, M62832; AAA1884.1; -.
DR F1R; A40522; A40522.
DR HSSP; P00747; 1PMK.
DR MEROPS; S01.233; -.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00051; Kringle_2.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle_2.
DR SMART; SM00130; KR_1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00740; KRINGLE_2; 2.
DR PROSITE; PS02040; TRYPSIN_DOM; PARTIAL.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.

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KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KM Tissue remodeling; Blood coagulation; Kringle; Repeat.
FT NON TER 1
FT DOMAIN <1 10 KRINGLE 3 (BY SIMILARITY).
FT DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
FT DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
FT DISULFID 34 112 BY SIMILARITY.
FT DISULFID 55 95 BY SIMILARITY.
FT DISULFID 83 107 BY SIMILARITY.
FT NON TER 169
SQ SEQUENCE 169 AA; 18401 MW; 77A54214C9D010C CRC64;

Query Match 47.9%; Score 243.5; DB 1; Length 169;
Best Local Similarity 48.2%; Pred. No. 3.3e-20;
Matches 41; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

QY 2 QDCMFGNGKGYRGKATTVTGPCEMAAOBPHRHSITPGINKAGIEKRYCRNPDGI 61
DB 32 QECYOGNGKSYRGTSSTNTGKCKQSWMTPHSHK-TPANFPDSDGEMNYCRNPDNDQ 90
QY 62 NGPWCYTMNPRKLPYCDIPLCAS 86
DB 91 RGPWCFTTDPVYRWBYCNLKRCSRT 115

RESULT 12
HGFL HUMAN
ID HGFL_HUMAN STANDARD; PRT; 711 AA.
AC P26927; Q13350; Q14870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP) (Macrophage stimulating protein).
GN MST1 OR HGFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92002016; PubMed=1655021;
RA Han S., Stuart L.A., Fritzen Degen S.J.;
RT "Characterization of the DNP152 locus on human chromosome 3:
RT identification of a gene coding for four kringle domains with
RT homology to hepatocyte growth factor.";
RL Biochemistry 30:9768-9780(1991).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93340141; PubMed=8393443;
RA Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
RT "Cloning, sequencing, and expression of human macrophage stimulating
RT protein (MSP, MST1) confirms MSP as a member of the family of Kringle
RT proteins and locates the MSP gene on chromosome 3.";
RL J. Biol. Chem. 268:15461-15468(1993).
CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
CC CONSERVED.
CC -1- PTM: MAY BE CLEAVED AFTER AA 484, TO YIELD A TWO-CHAIN MOLECULE
CC HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEPARATE POLYPEPTIDES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 4 kringle domains.
CC -----
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DR EMBL; M74178; AAA50165.1; -
DR EMBL; U37055; AAC50472.1; -
DR EMBL; L11924; AAA59872.1; -
DR PIR; A40331; A47136.
DR HSSP; P00747; 2PK4.
DR MEROPS; S01.975; -.
DR Genew; HGNC:7380; MST1.
DR MIM; 142408; -.
DR InterPro; IPR003314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser.protease_Try.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR Kringler; Glycoprotein; Serine protease homolog; Repeat; Signal;
KW Polymorphism.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 711 HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
FT DOMAIN 32 109 PAP.
FT DOMAIN 110 186 KRINGLE 1.
FT DOMAIN 191 268 KRINGLE 2.
FT DOMAIN 283 361 KRINGLE 3.
FT DOMAIN 370 448 KRINGLE 4.
FT DOMAIN 484 711 SERINE PROTEASE-LIKE.
FT DISULFID 56 78 BY SIMILARITY.
FT DISULFID 60 66 BY SIMILARITY.
FT DISULFID 110 186 BY SIMILARITY.
FT DISULFID 131 169 BY SIMILARITY.
FT DISULFID 157 181 BY SIMILARITY.
FT DISULFID 191 268 BY SIMILARITY.
FT DISULFID 194 324 INTERCHAIN (BY SIMILARITY).
FT DISULFID 212 251 BY SIMILARITY.
FT DISULFID 240 263 BY SIMILARITY.
FT DISULFID 283 361 BY SIMILARITY.
FT DISULFID 304 343 BY SIMILARITY.
FT DISULFID 332 355 BY SIMILARITY.
FT DISULFID 370 448 BY SIMILARITY.
FT DISULFID 391 431 BY SIMILARITY.
FT DISULFID 419 443 BY SIMILARITY.
FT DISULFID 468 588 INTERCHAIN (BY SIMILARITY).
FT DISULFID 507 523 BY SIMILARITY.
FT DISULFID 523 667 BY SIMILARITY.
FT DISULFID 602 646 BY SIMILARITY.
FT DISULFID 632 685 BY SIMILARITY.
FT CARBOHYD 72 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 13 13 Y -> C.
FT VARIANT 212 212 C -> F.
FT VARIANT 676 676 /FTID=VAR_006632.
FT VARIANT 676 676 E -> K (IN dSbNP:7798).
FT VARIANT 676 676 /FTID=VAR_014569.
FT CONFLICT 623 623 L -> F (IN REF. 2).
FT SEQUENCE 711 AA; 80379 MW; 596ED21F80290E4 CRC64;
Query Match 47.5%; Score 241.5; DB 1; Length 711;
Best Local Similarity 51.8%; Pred. No. 2.5e-19;
Matches 43; Conservative 11; Mismatches 28; Indels 1; Gaps 1;
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```
QY 2 ODCMFGNGKYGKATVTTGTPCQEWAAQEPHRHSFTIPGNNKAGLEKNTCRNPDGI 61
Db 368 QDCYHAGEGYGYGVTSKTRKGVQCQWASAEPTHK-PQFTFSBPHQLEHNCRNPDGS 426
QY 62 NGPWCYTNAPRKLPDYCDIPLCA 84
Db 427 HGFPCYMDPRTPFDYCALRCA 449

RESULT 13
HGFL MOUSE
ID HGFL_MOUSE STANDARD; PRT; 716 AA.
AC P26928;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP).
GN MST1 OR HGFL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=92002017; PubMed=1832957;
RA Friesner Degen S.J., Stuart L.A., Han S., Jamison C.S.;
RT "Characterization of the mouse cdna and gene coding for a hepatocyte
RT growth factor-like protein: expression during development.";
RL Biochemistry 30:9781-9791(1991).
CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
CC CONSERVED
CC -1- TISSUE SPECIFICITY: LIVER. LOWER LEVELS IN LUNG, PLACENTA AND
CC ADRENAL.
CC -1- DEVELOPMENTAL STAGE: IS EXPRESSED AT LOW LEVELS DURING GESTATION.
CC JUST BEFORE BIRTH THE LEVEL INCREASES DRAMATICALLY AND REMAINS
CC STABLE AFTERWARDS.
CC -1- PTM: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE
CC HELD TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE
CC POLYPEPTIDES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 4 kringle domains.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M74180; AAA50166.1; -
DR EMBL; M74181; AAA50167.1; -
DR PIR; A40332; A40332.
DR HSSP; P00747; 1XRN.
DR MEROPS; S01.975; -.
DR MCD; MGI:96080; Met1.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser.protease_Try.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
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DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; TRY SP; 1.
DR PROSITE; PS00021; KRINGLE 1; 4.
DR PROSITE; PS00070; KRINGLE 2; 4.
DR PROSITE; PS00240; TRYP SIN DOM; 1.
KW Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal.
FT CHAIN 1 18
FT DOMAIN 19 716
FT DOMAIN 19 109
FT DOMAIN 110 186
FT DOMAIN 191 268
FT DOMAIN 292 370
FT DOMAIN 379 457
FT DOMAIN 489 716
FT DISULFID 56 78
FT DISULFID 60 66
FT DISULFID 110 186
FT DISULFID 131 169
FT DISULFID 157 181
FT DISULFID 191 268
FT DISULFID 194 333
FT DISULFID 212 251
FT DISULFID 240 263
FT DISULFID 292 370
FT DISULFID 313 352
FT DISULFID 341 364
FT DISULFID 379 457
FT DISULFID 400 440
FT DISULFID 428 452
FT DISULFID 477 593
FT DISULFID 512 528
FT DISULFID 607 672
FT DISULFID 637 651
FT DISULFID 662 690
FT CARBOHYD 72 72
FT CARBOHYD 173 173
FT CARBOHYD 305 305
FT CARBOHYD 620 620
FT COMPACT 19 19
SQ SEQUENCE 716 AA; 80588 MW; B8C02EB85213ACC CRC64;

Query Match 47.1%; Score 239.5; DB 1; Length 716;
Best Local Similarity 48.8%; Pred. No. 4.2e-19;
Matches 40; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

QY 2 QDCMFGNGKYGKATVTGTPCOEAAOEPHRSFTIPGINKAGLEKRYCRNPDGI 61
DB 377 EGCYHSGSGYRGSVSKTRKGVCCQHMSSSTPHK-PQFTPTSPAPQALEANFCRNDGDS 435
QY 62 NGPWCTYMPNPKLFDCDIPLC 83
DB 436 HGPWCYLDLPDILFDYCALQRC 457

RESULT 14
APOA MACMU STANDARD; PRT; 1420 AA.
AC P14417;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment).
GN LPA.
OS Macaca mulatta (Rhesus macaque).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_Taxid=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89174660; PubMed=2925643;
RA Tomlinson J.E., McLean J.W., Lawn R.M.;
RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of

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RT synthesis."
RL J. Biol. Chem. 264:5957-5965(1989).
CC - FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
CC (Lp(a)). It has serine proteinase activity and is able of
CC autoproteolysis. Inhibits tissue-type plasminogen activator 1.
CC Lp(a) may be a ligand for megalin/Gp 330.
CC - SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
CC decorin (by similarity).
CC - PTM: N- and O-glycosylated (by similarity).
CC - DISEAS: Elevated plasma concentrations of apo(a) and its
CC naturally occurring proteolytic fragments are correlated with
CC atherosclerosis. Homology with plasminogen kringle IV and V is
CC thought to underlie the atherogenicity of the protein, because the
CC fragments are competing with plasminogen for fibrin(ogen) binding.
CC - MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
CC leading to the formation of the so called mini-Lp(a). Apo(a)
CC fragments accumulate in atherosclerotic lesions, where they may
CC promote thrombogenesis. O-glycosylation may limit the extent of
CC proteolytic fragmentation (by similarity).
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC - SIMILARITY: Contains at least 10 kringle domains.
CC -----
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CC -----
DR EMBL; J04635; AAA36833.1; -
DR PIR; A32869; A32869.
DR HSSP; P00747; 2PK4.
DR MEROPS; S01.226; -
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Ser protease_Try.
DR Pfam; PF00051; Kringle; 11.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 10.
DR SMART; SM00020; TRY SP; 1.
DR SMART; SM00021; KRINGLE 1; 10.
DR PROSITE; PS00070; KRINGLE 2; 10.
DR PROSITE; PS00240; TRYP SIN DOM; 1.
DR PROSITE; PS00135; TRYP SIN SER; FALSE NEG.
DR PROSITE; PS00135; TRYP SIN SER; FALSE NEG.
KW Hydrolase; Serine protease; Lipid transport; Plasma; Glycoprotein;
KW Kringle; Repeat; Atherosclerosis.
FT NON_TER 1 1
FT DOMAIN 49 127
FT DOMAIN 163 241
FT DOMAIN 277 355
FT DOMAIN 391 469
FT DOMAIN 505 583
FT DOMAIN 619 697
FT DOMAIN 725 803
FT DOMAIN 839 917
FT DOMAIN 953 1031
FT DOMAIN 1067 1145
FT DOMAIN 1191 1420
SQ SEQUENCE 1420 AA; 158367 MW; BE102949E03C580E CRC64;

Query Match 46.5%; Score 236; DB 1; Length 1420;
Best Local Similarity 49.4%; Pred. No. 2.1e-18;
Matches 42; Conservative 12; Mismatches 23; Indels 8; Gaps 3;

QY 2 QDCMFGNGKYGKATVTGTPCOEAAOEPHRSFTIPGINKAGLEKRYCRNPD 58
DB 724 QDCYHSGSGYRGSVSKTRKGVCCQHMSSSTPHK-PQFTPTSPAPQALEANFCRND 779

```

QY 59 GDINGPWCYTMNPKLFDCDPLC 83
 Db 780 AEIR-PWCYTMNPKLFDCDPLC 803

RESULT 15
 HGF_HUMAN STANDARD; PRT; 728 AA.

AC P14210; O98Y19; O9UDU6;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 DE (Hepatopoietin A).
 DE HGF OR HPTA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 [1]

RN SEQUENCE FROM N.A.
 RX MEDLINE=91340155; PubMed=1831432;
 RA Seki T., Hagiya M., Shimomishi M., Nakamura T., Shimizu S.;
 RT "Organization of the human hepatocyte growth factor-encoding gene.";
 RL Gene 102:213-219 (1991).
 [2]

RN SEQUENCE FROM N.A.
 RX TISSUE=Placenta;
 RA MEDLINE=9932017; PubMed=2528952;
 RA Miyazawa K., Teubouchi H., Naka D., Takahashi K., Okigaki M.,
 RA Atakaki N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,
 RA Gohda E., Daikuhara Y., Kitamura N.;
 RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
 growth factor.";
 RL Biochem. Biophys. Res. Commun. 163:967-973 (1989).
 [3]

RN SEQUENCE FROM N.A.
 RX TISSUE=Leukocyte;
 RA MEDLINE=91025062; PubMed=2145836;
 RA Seki T., Ihara I., Sugimura A., Shimomishi M., Nishizawa T.,
 RA Aami O., Hagiya M., Nakamura T., Shimizu S.;
 RT "Isolation and expression of cDNA for different forms of hepatocyte
 growth factor from human leukocyte.";
 RL Biochem. Biophys. Res. Commun. 172:321-327 (1990).
 [4]

RN SEQUENCE FROM N.A. AND SEQUENCE OF 55-73 AND 495-520.
 RX TISSUE=Liver;
 RA MEDLINE=9006676; PubMed=2531289;
 RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimomishi M.,
 RA Sugimura A., Tashiro K., Shimizu S.;
 RT "Molecular cloning and expression of human hepatocyte growth factor.";
 RL Nature 342:440-443 (1989).
 [5]

RN SEQUENCE FROM N.A.
 RX TISSUE=Embryonic fibroblast;
 RA MEDLINE=9134393; PubMed=1831266;
 RA Weidner K.M., Atakaki N., Hartmann G., Vandekerckhove J., Weingart S.,
 RA Rieder H., Fomatsch C., Teubouchi H., Hishida T., Daikuhara Y.,
 RA Birmeleier W.;
 RT "Evidence for the identity of human scatter factor and human
 hepatocyte growth factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005 (1991).
 [6]

RN SEQUENCE FROM N.A.
 RA Courtney L., Elliot G., Angel S.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 [7]

RN SEQUENCE OF 249-695 FROM N.A.
 RX MEDLINE=91369928; PubMed=1832556;
 RA Miyazawa K., Kitamura A., Kitamura N.;
 RT "Structural organization and the transcription initiation site of the
 human hepatocyte growth factor gene.";
 RL Biochemistry 30:9170-9176 (1991).

RN [8]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=9107365; PubMed=1826837;
 RA Yoshiyama Y., Atakaki N., Naka D., Takahashi K., Hirono S., Kondo J.,
 RA Nakayama H., Gohda E., Kitamura N., Teubouchi H., Ishii T.,
 RA Hishida T., Daikuhara Y.;
 RT "Identification of the N-terminal residue of the heavy chain of both
 RT native and recombinant human hepatocyte growth factor.";
 RL Biochem. Biophys. Res. Commun. 175:660-667 (1991).
 [9]

RN CARBOHYDRATE-LINKAGE SITE THR-476.
 RX MEDLINE=91329192; PubMed=1462348;
 RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
 RA Nakamura T., Shimizu S.;
 RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
 RT on the alpha chain.";
 RL Biochem. Biophys. Res. Commun. 189:1329-1335 (1992).
 [10]

RN MUTAGENESIS.
 RX MEDLINE=92331602; PubMed=1321034;
 RA Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
 RA Baker J.B., Godowski P.J.;
 RT "Structure-function analysis of hepatocyte growth factor:
 RT identification of variants that lack mitogenic activity yet retain
 RT high affinity receptor binding.";
 RL EMBO J. 11:2503-2510 (1992).
 [11]

RN STRUCTURE BY NMR OF 31-127.
 RX MEDLINE=98154323; PubMed=9493272;
 RA Zhou H., Mazzulla M.J., Kautman J.D., Stahl S.J., Wingfield P.T.,
 RA Rubin J.S., Bottaro D.P., Byrd R.A.;
 RT "The solution structure of the N-terminal domain of hepatocyte growth
 RT factor reveals a potential heparin-binding site.";
 RL Structure 6:109-116 (1998).
 [12]

RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.
 RX MEDLINE=99036858; PubMed=9817840;
 RA Ultsch M., Lokker N.A., Godowski P.J., de Vos A.M.;
 RT "Crystal structure of the NK1 fragment of human hepatocyte growth
 RT factor at 2.0-A resolution.";
 RL Structure 6:1183-1193 (1998).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 CC HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS
 CC AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUE AND CELL TYPES.
 CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 CC DISULFIDE BOND.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 4 kringle domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; D90334; BAA14348.1; -;
 DR EMBL; D90318; BAA14348.1; JOINED.
 DR EMBL; D90319; BAA14348.1; JOINED.
 DR EMBL; D90320; BAA14348.1; JOINED.
 DR EMBL; D90321; BAA14348.1; JOINED.
 DR EMBL; D90322; BAA14348.1; JOINED.
 DR EMBL; D90323; BAA14348.1; JOINED.
 DR EMBL; D90324; BAA14348.1; JOINED.
 DR EMBL; D90325; BAA14348.1; JOINED.
 DR EMBL; D90326; BAA14348.1; JOINED.
 DR EMBL; D90327; BAA14348.1; JOINED.
 DR EMBL; D90328; BAA14348.1; JOINED.
 DR EMBL; D90329; BAA14348.1; JOINED.
 DR EMBL; D90330; BAA14348.1; JOINED.
 DR EMBL; D90331; BAA14348.1; JOINED.
 DR EMBL; D90332; BAA14348.1; JOINED.

Search completed: January 12, 2004, 17:23:58
Job time : 8.43609 secs

DR EMBL; D90333; BAA14348.1; JOINED.
DR EMBL; M29145; AAAS2650.1; -.
DR EMBL; M60718; AAAS2648.1; -.
DR EMBL; X16323; CAA34387.1; -.
DR EMBL; M73239; AAA64239.1; -.
DR EMBL; M73240; AAA64297.1; -.
DR EMBL; AC004960; AAC71655.1; -.
DR EMBL; M75983; AAG53460.1; -.
DR EMBL; M75972; AAG53460.1; JOINED.
DR EMBL; M75973; AAG53460.1; JOINED.
DR EMBL; M75974; AAG53460.1; JOINED.
DR EMBL; M75975; AAG53460.1; JOINED.
DR EMBL; M75976; AAG53460.1; JOINED.
DR EMBL; M75977; AAG53460.1; JOINED.
DR EMBL; M75978; AAG53460.1; JOINED.
DR EMBL; M75979; AAG53460.1; JOINED.
DR EMBL; M75980; AAG53460.1; JOINED.
DR EMBL; M75981; AAG53460.1; JOINED.
DR EMBL; M75982; AAG53460.1; JOINED.
DR PIR; JH0579; JH0579.
DR PDB; 2HGF; 24-JUN-98.
DR PDB; 1BHT; 18-NOV-98.
DR PDB; 1NK1; 29-DEC-99.
DR MEROPS; S01.976; -.
DR GLYCOSULEDB; P14210; -.
DR Genew; HGNC:4893; HGF.
DR MIM; 142409; -.
DR GO; GO:0008083; F:Growth factor activity; NAS.
DR GO; GO:0007067; P:mitosis; NAS.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle; 4.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS0070; KRINGLE_2; 4.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
KW Signal; 3D-structure; Polymorphism; Pyroliidone carboxylic acid.
FT SIGNAL 1 31
FT CHAIN 32 494 HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
FT CHAIN 495 728 HEPATOCYTE GROWTH FACTOR BETA CHAIN.
FT MOD_RES 32 127 PYROLIDONE CARBOXYLIC ACID.
FT DOMAIN 32 127 PAP.
FT DOMAIN 128 206 KRINGLE 1.
FT DOMAIN 211 288 KRINGLE 2.
FT DOMAIN 305 383 KRINGLE 3.
FT DOMAIN 391 469 KRINGLE 4.
FT DOMAIN 495 728 SERINE PROTEASE-LIKE.
FT DISULFID 70 96
FT DISULFID 74 84
FT DISULFID 128 206

Query Match 46.2%; Score 234.5; DB 1; Length 728;
Best Local Similarity 43.4%; Pred. No. 1.5e-18;
Matches 36; Conservative 19; Mismatches 27; Indels 1; Gaps 1;

QY 2 ODCMFGNGKGYRGKKAATYTVTGTCQEAQEPHRHSFTPTGNTKMAGLEKNGCRNPDGDI 61
DB 126 RNCITLKGKRSYKGVSTVSTSGICQCPWSSMTIPIHNS-FLPSSYRGKDLQENTCRNPRGEE 184
QY 62 NGPMCYTMNPKLFDYCDIPLCA 84
DB 185 GGPWCFTSNPEVRYEVCIDIPOCS 207

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:18:07 : Search time 27.4812 Seconds
(without alignments)
807.553 Million cell updates/sec

Title: US-10-088-548-8
Perfect score: 508
Sequence: 1 EDDCMFGNGKGYRKATTVT.....YTMNPKLPDYCDIPICASS 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp Unclassified: *
15: sp_rvivirus: *
16: sp_bacteriaph: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	501	98.6	95	4 Q8N696	Q8N696 homo sapien
2	430	84.6	810	4 Q15146	Q15146 homo sapien
3	413	81.3	812	11 Q91WJ5	Q91WJ5 mus musculu
4	408	80.3	812	11 Q9ROW3	Q9ROW3 ractus novy
5	404	79.5	334	6 O46507	O46507 papio hamed
6	379	74.6	806	6 O18783	O18783 macropus eu
7	285	56.1	429	13 Q8AVB0	Q8AVB0 brachydantio
8	250.5	49.3	359	6 Q8WNR1	Q8WNR1 canis fam11
9	246.5	48.5	313	13 Q9PU78	Q9PU78 crocodylus
10	243.5	47.9	716	11 P70521	P70521 ractus novy
11	240.5	47.3	709	13 Q9QZM6	Q9QZM6 brachydantio
12	239.5	47.1	716	11 Q91XG8	Q91XG8 mus musculu
13	239	47.0	2869	6 Q28398	Q28398 etinaceus e
14	237.5	46.8	567	4 Q13308	Q13308 homo sapien
15	237.5	46.8	710	13 Q91402	Q91402 xenopus. he
16	236.5	46.6	209	11 Q8BS17	Q8BS17 mus musculu

17	236	46.5	454	6 O46506	O46506 papio hamed
18	234.5	46.2	208	4 Q9BYM0	Q9BYM0 homo sapien
19	234.5	46.2	210	4 Q13494	Q13494 homo sapien
20	234.5	46.2	290	4 Q02935	Q02935 homo sapien
21	234.5	46.2	296	4 Q14519	Q14519 homo sapien
22	233.5	46.0	704	13 Q90865	Q90865 gallus gall
23	232	45.7	105	4 Q9URR8	Q9URR8 homo sapien
24	231.5	45.6	90	4 Q8NG20	Q8NG20 homo sapien
25	230	45.3	113	4 Q9URR7	Q9URR7 homo sapien
26	230	45.3	113	4 Q9URR5	Q9URR5 homo sapien
27	227.5	44.8	109	6 Q9N1B8	Q9N1B8 ovis aries
28	227.5	44.8	211	11 Q55027	Q55027 mus musculu
29	227.5	44.8	728	6 Q9BH09	Q9BH09 felis silve
30	227.5	44.8	728	11 Q8C9G5	Q8C9G5 mus musculu
31	224	44.1	145	6 Q28911	Q28911 macaca fasc
32	222.5	43.8	726	13 Q90978	Q90978 gallus gall
33	217	42.7	113	4 Q9URR6	Q9URR6 homo sapien
34	216	42.5	285	4 Q8TCR2	Q8TCR2 homo sapien
35	214	42.1	132	4 Q16609	Q16609 homo sapien
36	212	41.7	648	4 Q9H1V4	Q9H1V4 homo sapien
37	211.5	41.6	716	13 Q91691	Q91691 xenopus lae
38	205.5	40.5	717	13 P70006	P70006 xenopus lae
39	201	39.6	385	5 Q25101	Q25101 herdamia m
40	199.5	39.3	948	5 Q9Y1Y6	Q9Y1Y6 ephydactia f
41	196.5	38.7	801	11 Q8K0Q8	Q8K0Q8 mus musculu
42	196.5	38.7	944	11 Q8C3W2	Q8C3W2 mus musculu
43	196.5	38.7	944	11 Q8BSR6	Q8BSR6 mus musculu
44	193.5	38.1	215	13 Q42341	Q42341 gallus gall
45	192.5	37.9	930	13 Q8AV69	Q8AV69 xenopus lae

ALIGNMENTS

RESULT 1

Q8N696 PRELIMINARY; PRT; 95 AA.
ID Q8N696
AC Q8N696;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Antiangiogenic AK38 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Dou D.;
RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
RL -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
CC EMBL, AY039748; AAK74187.1; -.
DR EMBL; IPR000001; Kringle.
DR InterPro; IPR003966; Prothrombin.
DR Pfam; PF00051; Kringle_1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
KW Glycoprotein; Kringle.
SQ
SEQUENCE 95 AA; 10553 MW; 31EDC9DB38A372DF CRC64;

Query Match 98.6%; Score 501; DB 4; Length 95;
Best Local Similarity 98.8%; Pred. No. 1.8e-50;

Matches 84; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDDCMFGNGKGYRKATTVTGTPCQEWAAQEPHRSFTFIPCTNKAGLEKXKNCNPDGD 60
Db 11 EDDCMFGNGKGYRKATTVTGTPCQEWAAQEPHRSFTFIPCTNKAGLEKXKNCNPDGD 70

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QY 61 INGPWCYTMNPKLFDYCDIPLCAS 85
DB 71 INGPWCYTMNPKLFDYCDIPLCAA 95

RESULT 2
ID Q15146 PRELIMINARY; PRT; 810 AA.
AC Q15146;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasmalogen precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
RA Mitchell D., Robinson J.H.;
RT "Expression of recombinant human plasmalogen and aglycoplaaminogen in
RT HeLa cells.";
RL Fibrinolysis 0:0-0(1991).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
EMBL: M74220; AAA36451.1; -.
DR HSSP; P00747; 2PK4.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; KRINGLE; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN Ap; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS50070; KRINGLE_2; 5.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 810 PLASMINOGEN.
SQ SEQUENCE 810 AA; 90555 MW; B05C7D4BD020B3C CRC64;

Query Match 84.6%; Score 430; DB 4; Length 810;
Best Local Similarity 82.4%; Pred. No. 3.4e-41;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATVTTGTPCOEWAQEPHRSHTFPGTNKWALEKNCYCRNPDDG 60
DB 478 EBDGMPGNGKGYRGKATVTTGTPCOEWAQEPHRSHTFPGTNKWALEKNCYCRNPDDG 537

QY 61 INGPWCYTMNPKLFDYCDIPLCAS 85
DB 538 VGGPWCYTMNPKLFDYCDIPLCAA 562

RESULT 3
Q15WJ5 PRELIMINARY; PRT; 812 AA.
AC Q15WJ5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasmalogen.
GN PLG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Bratwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA Nagaraia R.;
RT "Genomic Sequence Analysis in the Mouse t-complex Region.";
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
EMBL: BC014773; AAH14773.1; -.
DR EMBL; AF481053; AAM22156.1; -.
DR HSSP; P00761; IAN1.
DR MGD; MGI:97620; Plg.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; KRINGLE_1; 5.
DR PROSITE; PS00021; KRINGLE_2; 5.
DR PROSITE; PS50070; KRINGLE_2; 5.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 812 AA; 90781 MW; 2417326BE6A2FED2 CRC64;

Query Match 81.3%; Score 413; DB 11; Length 812;
Best Local Similarity 80.2%; Pred. No. 3.1e-39;
Matches 69; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATVTTGTPCOEWAQEPHRSHTFPGTNKWALEKNCYCRNPDDG 60
DB 478 ETCOMGNGKGYRGKATVTTGTPCOEWAQEPHRSHTFPGTNKWALEKNCYCRNPDDG 537

QY 61 INGPWCYTMNPKLFDYCDIPLCAS 86
DB 538 VGGPWCYTMNPKLFDYCDIPLCAA 563

RESULT 4
Q15WJ5 PRELIMINARY; PRT; 812 AA.
AC Q15WJ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasmalogen protein precursor (EC 3.4.21.7).
GN PLASMINOGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Bangert K., Johnsen A.H., Thorsen S.;
RT "Rat plasminogen: cDNA and gene structure.";
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=91250378; PubMed=1645711;
RA Kanalaas J.U., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen.";
RL J. Biol. Chem. 266:10825-10829(1991).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL: AJ242649; CAB46014.1; -.
DR HSSP: P00747; 1PMK.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan app.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00051; Kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR ProDom: PD000395; Kringle; 5.
DR SMART: SM00130; KR; 4.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00021; KRINGLE_1; 5.
DR PROSITE: PS00070; KRINGLE_2; 5.
DR PROSITE: PS00338; SOMATOSTATIN_2; 1.
DR PROSITE: PS0240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR GlycoProtein; Hydrolase; Kringle; Protease; Serine protease; Signal.
FT SIGNAL
FT CHAIN
FT FT
SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410EBC9E CRC64;

Query Match 80.3%; Score 408; DB 11; Length 812;
Best Local Similarity 80.0%; Pred. No. 1.2e-38;
Matches 68; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 BDCMFGNGKGYRGKATVTGTPCQEMAAQEPHSHSTFGTNKMAGLEKMYCRNPDGD 60
DB 478 EIDCMGNGKGYRGKATVTGTPCQEMAAQEPHSHSTFGTNKMAGLEKMYCRNPDGD 537

QY 61 INGPWCYTANPRKLFYDCIPIPLCASS 85
DB 538 VNGPWCYTANPRKLFYDCIPIPLCASS 562

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RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cox L.A., Jett C., Hixson J.E.;
RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
RT Site Mutation is Associated with Deletion of a Single Exon in a Null
RT Allele.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL: AF029692; AAB97887.1; -.
DR HSSP: P00747; 5HPG.
DR MEROPS: S01.233; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00051; Kringle; 1.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00024; PAN; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR ProDom: PD000395; Kringle; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
DR PROSITE: PS0240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR GlycoProtein; Hydrolase; Kringle; Protease; Serine protease.
FT NON TER
FT FT
SQ SEQUENCE 334 AA; 36791 MW; C7DC06E03B965286 CRC64;

Query Match 79.5%; Score 404; DB 6; Length 334;
Best Local Similarity 81.0%; Pred. No. 1.3e-38;
Matches 68; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 3 DCMFGNGKGYRGKATVTGTPCQEMAAQEPHSHSTFGTNKMAGLEKMYCRNPDGD 62
DB 4 DCMFGNGKGYRGKATVTGTPCQEMAAQEPHSHSTFGTNKMAGLEKMYCRNPDGD 63

QY 63 GPWCYTANPRKLFYDCIPIPLCASS 86
DB 64 GPWCYTANPRKLFYDCIPIPLCASS 87

RESULT 6
O18783
ID O18783 PRELIMINARY; PRT; 806 AA.
AC O18783;
DT 01-JAN-1998 (TRENBLREL. 05, Created)
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Plasminogen.
OS Macropus eugenii (Tammam wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCB1_Taxid=9315;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=98004511; PubMed=9342350;
RA Law R.M., Schwartz K., Patchy L.;
RT "Convergent evolution of Apolipoprotein(a) in primates and hedgehog.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL: AF012297; AAB65760.1; -.
DR HSSP: P00747; 5HPG.
DR MEROPS: S01.233; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan app.
DR InterPro: IPR003966; Prothrombin.

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DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF000051; kringle_5.
 DR Pfam: PF00024; PAN_1.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle_5.
 DR SMART: SM00130; KR_4.
 DR SMART: SM00473; PAN_Ap_1.
 DR SMART: SM00020; TRYP_Spc_1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS00134; TRYPsin_Dom_1.
 DR PROSITE: PS00135; TRYPsin_HIS_1.
 DR PROSITE: PS00135; TRYPsin_SER_1.
 DR GlycoProtein: Hydrolyase; Kringle; Protease; Serine protease.
 SW SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;

Query Match 74.6%; Score 379; DB 6; Length 806;
 Best Local Similarity 74.1%; Pred. No. 2.7e-35;
 Matches 63; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATVTGTGTCQEWAAQEPHRSFTFGTNKMALEKNYCRNPDGD 60
 DB 473 ESDCMGSGKDYRGKSTVTGTLCAQMTAEPRHRTIFPDYTPRAGLEENTCRNPDGD 532
 QY 61 INGPWCYTNMPKLFYCDIPLCAS 85
 DB 533 PNGPWCYTNMPKLFYCDIPLCAS 557

RESULT 7

ID Q8AVB0 PRELIMINARY; PRT; 429 AA.
 AC Q8AVB0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Plasmidogen precursor (Fragment).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hanumanthiah R., Day K., Jagadeeswaran P.;
 RT "Comprehensive analysis of blood coagulation pathways in teleostei;
 RT Evolution of coagulation factor genes and identification of zebrafish
 RT factor VIII.";
 RL Blood Cells Mol. Dis. 0:0-0(2002).
 DR EMBL; AF515276; NAN71006.1; -.
 FT NON_TER 1
 SQ SEQUENCE 429 AA; 47556 MW; 9A580A214A549C12 CRC64;

Query Match 56.1%; Score 285; DB 13; Length 429;
 Best Local Similarity 55.3%; Pred. No. 1e-24;
 Matches 47; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATVTGTGTCQEWAAQEPHRSFTFGTNKMALEKNYCRNPDGD 60
 DB 99 EKDCKNGNGAEYRSGTSMNTMGVTCQAMRSMTFHQHASFTPEHPDKGLSNGCRNPDSD 158
 QY 61 INGPWCYTNMPKLFYCDIPLCAS 85
 DB 159 VNGPWCYTTDPBSKMDYCOIPDCS 183

RESULT 8
 Q8WMR1
 ID Q8WMR1 PRELIMINARY; PRT; 359 AA.
 AC Q8WMR1;

DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Plasmidogen (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pirie-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,
 RA Folkmann J., Waters D.J.;
 RT "Angiotensin is detectable in the urine of dogs with spontaneous Bone
 RT Cancer.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC EMBL; AY069985; AAL58519.1; -.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003966; Prothrombin.
 DR Pfam: PF00051; Kringle_4.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; KRINGLE.
 DR SMART: SM00130; KR_4.
 DR PROSITE: PS00021; KRINGLE_1; 4.
 DR PROSITE: PS00070; KRINGLE_2; 4.
 KW Glycoprotein; Kringle.
 FT NON_TER 1
 FT NON_TER 359
 SQ SEQUENCE 359 AA; 41172 MW; 776D35F4AB0BDD9E CRC64;

Query Match 49.3%; Score 250.5; DB 6; Length 359;
 Best Local Similarity 53.1%; Pred. No. 8.4e-21;
 Matches 43; Conservative 8; Mismatches 29; Indels 1; Gaps 1;

QY 3 DCMFGNGKGYRGKATVTGTGTCQEWAAQEPHRSFTFGTNKMALEKNYCRNPDGDIN 62
 DB 5 ECKTGNGKTYRGTMATKNDVACQKWDNSPHK-PYTPKPHLEGLBENYCRNPDNDEN 63
 QY 63 GPCWCTYTNMPKLFYCDIPLC 83
 DB 64 GPCWCTYTNMPKLFYCDIPLC 84

RESULT 9

ID Q9PU78 PRELIMINARY; PRT; 313 AA.
 AC Q9PU78;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hepatocyte growth factor-like protein (Fragment).
 OS Crocodylus niloticus (Nile crocodile) (African crocodile).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylia; Crocodylinae; Crocodylus.
 NCBI_TaxID=8501;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Liver;
 RX MEDLINE=20022983; PubMed=10555283;
 RA Hughes S., Zelus D., Mouchiroud D.;
 RT "Warm-blooded isochoire structure in nile crocodile and turtle.";
 RL Mol. Biol. Evol. 16:1521-1527(1999).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; AF011396; CAB56422.1; -.
 DR HSSP; P00747; IHPU.
 DR MEROPS; S01.977; -.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00051; Kringle_2.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00018; KRINGLE.

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Qy      2  QDCMFNGKGVKRGKATVTTGTPCOEWAQOEPRHSTFFIPGNTKNMAGLEKKNYCNRPDGI 61
Db      377  EGCYHSGSGEGRVGSVSTRKGVQCOHMSSETPHK-PQFTPTSAAPHAGLEAFNCNRPDGS 435
Qy      62  NGPCYTMNPRKLFDYCDIPLC 83
Db      436  HGPWCYTLDEPTLFDYCALRKC 457

RESULT 11
Q90ZN6  PRELIMINARY;  PRT;  709 AA.
ID  Q90ZN6
AC  Q90ZN6
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Hepatocyte growth factor-like 1.
GN  Mst1 OR HGFL.
OS  Brachydanio rerio (Zebrafish) (Danio rerio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Danio.
OX  NCBI_TaxId=7955;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Baasert D.I., Wilson S.W.;
RT  "Early expression of zebrafish Hepatocyte Growth Factor-Like 1
RL  suggests a conserved role in vertebrate neural induction.";
RT  Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 51.
CC  -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR  EMBL; AF370035; AAK54207.1; -.
DR  HSSP; P00761; IAN1.
DR  ZFIN; ZDB-GENE-020806-3; mst1.
DR  InterPro; IPR001314; Chymotrypsin.
DR  InterPro; IPR000001; Kringle.
DR  InterPro; IPR003014; PAN.
DR  InterPro; IPR003609; Pan_app.
DR  InterPro; IPR001254; Ser_protease_Try.
DR  Pfam; PF00051; kringle; 4.
DR  Pfam; PF00024; PAN_1.
DR  Pfam; PF00089; trypsin_1.
DR  PRINTS; PR00722; CHYMOTRYPSIN.
DR  PRINTS; PR00018; KRINGLE.
DR  ProDom; PD000395; Kringle; 4.
DR  SMART; SM00473; PAN_AP; 1.
DR  SMART; SM00420; TRY_PSP; 1.
DR  SMART; SM00021; KRINGLE_1; 4.
DR  PROSITE; PS50070; KRINGLE_2; 4.
DR  PROSITE; PS50240; TRYPSIN_DOM; 1.
KM  Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ  SEQUENCE 709 AA; 81271 MW; 9907236C5DB73A20 CRC64;

Query Match 47.3%; Score 240.5; DB 13; Length 709;
Best Local Similarity 51.2%; Pred. No. 2,6e-19;
Matches 41; Conservative 12; Mismatches 24; Indels 3; Gaps 1;

Qy      4  CMFGNGKGVKCAKATVTTGTPCOEWAQOEPRHSTFFIPGNTKNMAGLEKKNYCNRPDGI 63
Db      111  CTVGKGDYGVKAVSTTSGRTCCQWMSKPFHDKRWTPSAIN--GLELNTCRNPDGDRIG 167
Qy      64  PWCYTMNPRKLFDYCDIPLC 83
Db      168  PWCYTMNPRKLFDYCDIPLC 83

RESULT 12

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O91XG8
ID O91XG8 PRELIMINARY; PRT; 716 AA.
AC O91XG8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hepatocyte growth factor-like.
GN HGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL; BC010551; AAH10551.1; -.
DR HSSP; P00761; 1AN1.
DR MGD; MGI:96080; Hgf1.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYF_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
KW SEQUENCE 716 AA; 80693 MW; 1247C48A7D4B4D CRC64;
SQ

Query Match 47.1%; Score 239.5; DB 11; Length 716;
Best Local Similarity 48.8%; Pred. No. 3.4e-19;
Matches 40; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

OY 2 QDCMFGNGKGYRGKATVTGTPCQEWAAQEPHSHSTFIPTNKMAGLEKNYCRNPDGDI 61
DB 377 EGCYHSGEGYRGSVSKTRKGVQCQHWSSSTPHK-PQFTPTSAFQAGLEANFCRNPDGDS 435
OY 62 NGPMCTYMNPRKLFYDCIPLCASS 86
DB 436 HGPWCYTLDPDILFDYCALQRC 457

RESULT 13
O28398 PRELIMINARY; PRT; 2869 AA.
ID O28398
AC O28398;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
OS Erinnaceus eurpaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96025778; PubMed=7592597;
RA Lawn R.M., Boommark N.W., Schwartz K., Lindahl G.E., Wade D.P.,

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RA Byrne C.D., Fong K.J., Meer K., Patchy L.;
RT "The recurring evolution of lipoprotein(a). Insights from cloning of
RT hedgehog apolipoprotein(a)."
RL J. Biol. Chem. 270:24004-24009(1995).
CC -1- SIMILARITY: CONTAINS 31 KRINGLE DOMAINS.
DR EMBL; U33170; AAC48522.1; -.
DR HSSP; P00747; 1PMK.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 31.
DR PRINTS; PRO0018; KRINGLE.
DR PRODOM; PD000395; Kringle; 31.
DR SMART; SM00130; KR; 31.
DR PROSITE; PS00021; KRINGLE_1; 30.
DR PROSITE; PS50070; KRINGLE_2; 31.
KW Glycoprotein; Kringle; Lipoprotein.
FT NON TER 1
SQ SEQUENCE 2869 AA; 318601 MW; 9527CEP985A4FB2A CRC64;

Query Match 47.0%; Score 239; DB 6; Length 2869;
Best Local Similarity 50.6%; Pred. No. 1.8e-18;
Matches 43; Conservative 9; Mismatches 31; Indels 2; Gaps 2;

OY 2 QDCMFGNGKGYRGKATVTGTPCQEWAAQEPHSHSTFIPTNKMAGLEKNYCRNPDGDI 61
DB 2589 EGCLENGENGYQNMATVSGPCQGRKQTPHRH-YTPENYPSKNLFGNFCRNPDGDI 2647
OY 62 NGPMCTYMNPRKLFYDCIPLCASS 86
DB 2648 -APWCYTNASVAVRWECSIPTCESS 2671

RESULT 14
O13208 PRELIMINARY; PRT; 567 AA.
ID O13208
AC O13208;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hepatocyte growth factor-like protein homolog.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20191171; PubMed=10728827;
RA Degen S.-J.F., McDowell S.A., Waltz S.B., Gould F., Stuart L.A.,
RA Caritic B.;
RT "Structure of the human DIP151A locus: a chromosome 1 locus with 978
RT identity to the chromosome 3 gene coding for hepatocyte growth factor-
RT like protein."
RL DNA Seq. 8:409-413(1998).
CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL; U28054; AAC63092.1; -.
DR HSSP; P00747; 2PK4.
DR MEROPS; S01.977; -.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00020; TRYF_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 3.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 567 AA; 64117 MW; 3FC38B07F1645810 CRC64;

Query Match 46.8%; Score 237.5; DB 4; Length 567;
Best Local Similarity 50.6%; Pred. No. 4.5e-19;

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Matches 42; Conservative 12; Mismatches 28; Indels 1; Gaps 1;

QY 2 QDCMFGNGKGYRGKATTTVTGTCQEMAAQEPHRHSTFIPTNKWAGLEKNYCRNPDDGI 61
 DB 343 QDCIHHKGSNTYRGTNRVTKRGLACQPMNSMIPHEHS-FLPSTYRGKDLKENYCRNPKGBE 171
 QY 62 NGPMCTYMNPRKLDYCDIPLCA 84
 DB 402 HGPWCYTMDBRTPFDYCALRCA 424

RESULT 15

Q91402 PRELIMINARY; PRT; 710 AA.
 ID Q91402;
 AC Q91402;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hepatocyte growth factor.
 GN HGF.
 OS Xenopus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae.
 OC NCBI_TaxID=8353;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tail bud;
 RX MEDLINE=95267690; PubMed=7748783;
 RA Nakamura H., Tashiro K., Nakamura T., Shiohawa K.;
 RT "Molecular cloning of Xenopus HGF cDNA and its expression studies in
 RT Xenopus early embryogenesis";
 RL Mech. Dev. 49:123-131(1995)
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 DR EMBL: S77422; AAB34354.2; -.
 DR HSSP: P14210; 1BHT.
 DR MEROPS: S01.976; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00051; kringle; 4.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 4.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRY_SPC; 1.
 DR PROSITE: PS00021; KRINGLE_1; 4.
 DR PROSITE: PS50070; KRINGLE_2; 4.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 KM Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 710 AA; 81487 MW; 5FE6480BE31C27FC CRC64;

Query Match 46.8%; Score 237.5; DB 13; length 710;
 Best local Similarity 47.0%; Pred. No. 5.8e-19;
 Matches 39; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

QY 2 QDCMFGNGKGYRGKATTTVTGTCQEMAAQEPHRHSTFIPTNKWAGLEKNYCRNPDDGI 61
 DB 113 RDCIHHKGSNTYRGTNRVTKRGLACQPMNSMIPHEHS-FLPSTYRGKDLKENYCRNPKGBE 171
 QY 62 NGPMCTYMNPRKLDYCDIPLCA 84
 DB 172 GGPWCYTMDBRTPFDYCALRCA 424

Search completed: January 12, 2004, 17:25:37
 Job time : 27.4812 secs

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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:16:07 ; Search time 34.2707 Seconds
(without alignments)
398.314 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508
Sequence: 1 BDDCMFGNGKGRKKATTV.....YTMNPKLFDYCDIPLCASS 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*
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16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	86	22	AA172947 Human apolipoprotein
2	508	100.0	91	20	AA142303 Human apolipoprotein
3	508	100.0	308	22	AA172944 Human angiotensin
4	432	85.0	380	13	AA225044 [GARSQ] - [Plasmino
5	432	85.0	476	13	AA22503 [GARSQ] - [Plasmino
6	432	85.0	810	22	AA67228 Amino acid sequenc
7	430	84.6	90	21	AA601914 Human plasminogen
8	430	84.6	91	21	AA58868 Human plasminogen
9	430	84.6	93	21	AA601917 Human plasminogen

10	430	84.6	95	21	AA601913 Human plasminogen
11	430	84.6	98	21	AA601916 Human plasminogen
12	430	84.6	101	18	AA34286 Human kring 5 pe
13	430	84.6	101	21	AA601890 Human plasminogen
14	430	84.6	101	21	AA601912 Human plasminogen
15	430	84.6	104	21	AA601915 Human plasminogen
16	430	84.6	189	21	AA601918 Human plasminogen
17	430	84.6	192	21	AA601919 Human plasminogen
18	430	84.6	266	22	AAU32126 Novel human secret
19	430	84.6	266	22	AAU32129 Novel human secret
20	430	84.6	266	22	AAU32136 Novel human secret
21	430	84.6	271	21	AA608407 A human angiotens
22	430	84.6	348	23	ABB81498 Human miniplasmin
23	430	84.6	357	23	AA625408 Human tissue facto
24	430	84.6	362	23	ABB09586 Antiangiogenic fus
25	430	84.6	437	19	AA651457 Human plasminogen
26	430	84.6	484	24	AA679749 Human plasminogen
27	430	84.6	566	20	AA602100 A multifunctional
28	430	84.6	790	15	AA660519 Human 'Glu' plasmi
29	430	84.6	790	22	AA636562 Mammalian kring
30	430	84.6	791	21	AA601887 Human plasminogen
31	430	84.6	791	21	AA69589 Human plasminogen
32	430	84.6	791	21	AA650867 Human plasminogen
33	430	84.6	791	22	AA667223 Amino acid sequenc
34	430	84.6	791	23	AA623660 Human plasminogen
35	430	84.6	791	24	ABG76087 Human plasminogen
36	430	84.6	810	11	AA608065 Human plasminogen
37	430	84.6	810	12	AA612938 Plasminogen mutcin
38	430	84.6	810	14	AA634428 Sequence encoded b
39	430	84.6	810	20	AA608685 Human plasminogen
40	430	84.6	810	20	AA602114 SEQ ID 77 of WO91
41	430	84.6	810	21	AA682690 Human plasminogen
42	430	84.6	810	21	AA653867 Amino acid sequenc
43	430	84.6	810	23	ABB81470 Human plasminogen
44	430	84.6	810	23	ABB81496 Human plasminogen
45	430	84.6	810	23	ABB83795 Human plasminogen

ALIGNMENTS

RESULT 1
ID AA172947 standard; Protein; 86 AA.
AA172947;
XX
AC
XX
XX
DT 13-JUN-2001 (first entry)
XX
DE Human apolipoprotein(a) kring 5 domain V38, LK8 protein.
XX
XX Human; angiotensin inhibitor; LK8; apolipoprotein(a) kring 5 domain;
KW angiotensin-mediated disease; cancer; rheumatoid arthritis; therapy;
KW cystostatic; antithrombotic; antineoplastic; antipsoriatic; psoriasis;
KW ocular angiogenic disease; endothelial cell proliferation; tumour;
cell migration.
XX
XX Homo sapiens.
OS
XX
XX WO200119868-A1.
PN
XX
XX 22-MAR-2001.
PD
XX
XX 15-SEP-1999; 99WO-KR00554.
PF
XX
XX 15-SEP-1999; 99WO-KR00554.
PR
XX
XX 15-SEP-1999; 99WO-KR00554.
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
XX
XX Chang J, Kim JS, Park EJ, Yum J, Chung S;
PI WPI; 2001-244787/25.
DR N-PSDB; AAD03258.

XX Novel angiogenesis inhibitor. LK68 for treating angiogenesis-mediated
PT diseases, e.g. cancer and rheumatoid arthritis, has human
PT apolipoprotein(a) kringles IV36, IV37 and V38 amino acid
PT sequence -

PS Claim 3; Page 47; 50pp; English.

CC The present sequence is human LK6 protein which contains the amino
CC acid sequence of human apolipoprotein(a) kringles domain V38
CC (KV38). The human apolipoprotein(a) kringles domains IV36 (LK6
CC protein), IV37 (LK7 protein) and V38 (LK8 protein) together form the
CC angiogenesis inhibitor. LK68 protein. LK68, LK6, LK7 and LK8 are
CC inhibitors of endothelial cell proliferation, cell migration and
CC normal development of capillaries in the chick embryo chorioallantoic
CC membrane (CAM). LK68 protein, its single kringles or their functional
CC equivalents, are useful for treating angiogenesis-mediated diseases,
CC such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
CC disease in animals or humans. LK68 is useful as an anticancer agent and
CC also for inhibiting primary tumour growth.

SQ Sequence 86 AA;

Query Match 100.0%; Score 508; DB 22; Length 86;
Best Local Similarity 100.0%; Pred. No. 1e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EODCMFGNGKGYGKATTTGTPCOEWAQBPBRHSTFTPTNKVAGLEKATCRPPDD 60
DB 1 EODCMFGNGKGYGKATTTGTPCOEWAQBPBRHSTFTPTNKVAGLEKATCRPPDD 60

OY 61 INGPWCYTNNPKRLFDYCDIPLCASS 86
DB 61 INGPWCYTNNPKRLFDYCDIPLCASS 86

RESULT 2

AAV42303
ID AAV42303 standard; protein; 91 AA.

AC AAV42303;

DT 06-DEC-1999 (first entry)

DE Human apolipoprotein A kringles 5 domain.

KW Apolipoprotein A; apo(a); glycoprotein; heart disease; antibody;
KM detection; diagnosis.

OS Homo sapiens.

XX MO9936784-A1.

PD 22-JUL-1999.

PF 20-JAN-1999; 99WO-US01211.

PR 20-JAN-1998; 98US-0072924.

PA (ABBO) ABBOTT LAB.

PI Kundu SK, Ziemann R;

DR WPI; 1999-571560/48.

XX New methods for measuring concentrations of lipoprotein(a) in a plasma
PT sample -

PS Disclosure; Page 68; 71pp; English.

CC This sequence represents the kringles 5 domain of human apolipoprotein A
CC (apo(a)), which was used to generate monoclonal antibodies. Apo(a) is a
CC characteristic glycoprotein component of lipoprotein(a) (Lp(a)), which

CC is not found in the otherwise identical low density lipoprotein (LDL).
CC Lp(a) and LDL are both associated with premature coronary heart disease.
CC Increased Lp(a) concentrations may inhibit fibrinolysis by reducing the
CC generation of plasmin. This may be effected by competition for
CC plasminogen cell-surface receptors, by inhibition of activation of
CC antibodies can be used in a novel method of Lp(a) quantitation. Such
CC antibodies are not cross-reactive with plasminogen, LDL, and the various
CC types of apo(a) kringles 4 domains. Previous methods of Lp(a) immunoassay
CC used antibodies that bind to the apo(a) kringles 4 domain, which is
CC present in multiple copies. One method, TERUMO ELISA (enzyme-linked
CC immunosorbent assay), tended to produce erroneous results with cardiac
CC and diabetic patients, especially those with very high Lp(a)
CC concentrations (greater than 50 mg/dl). Apo(a) monoclonal antibodies may
CC serve as accurate markers for the detection and diagnosis of heart
CC disease.

SQ Sequence 91 AA;

Query Match 100.0%; Score 508; DB 20; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EODCMFGNGKGYGKATTTGTPCOEWAQBPBRHSTFTPTNKVAGLEKATCRPPDD 60
DB 3 EODCMFGNGKGYGKATTTGTPCOEWAQBPBRHSTFTPTNKVAGLEKATCRPPDD 62

OY 61 INGPWCYTNNPKRLFDYCDIPLCASS 86
DB 63 INGPWCYTNNPKRLFDYCDIPLCASS 88

RESULT 3

AAV72944
ID AAV72944 standard; protein; 308 AA.

AC AAV72944;

DT 13-JUN-2001 (first entry)

DE Human angiogenesis inhibitor, LK68 protein.

KW Human; angiogenesis inhibitor; LK68; apolipoprotein(a) kringles domain;
KM angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy;
KM cytostatic; antineumatic; antiarthritic; antipsoriatic; psoriasis;
KM ocular angiogenic disease; endothelial cell proliferation; tumour;
KM cell migration.

OS Homo sapiens.

XX MO200119868-A1.

XX 22-MAR-2001.

PF 15-SEP-1999; 99WO-KR00554.

PR 15-SEP-1999; 99WO-KR00554.

PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

[illegible]

XX		(BREC) BEECHAM GROUP PLC.	
PA	Dodd I , Brown M, Robinson JH;		
XX	WP1; 1992-114357/14.		
DR			
PT	Hybrid plasminogen activators for treating thrombotic diseases -		
PR	comprise Kringles 5 or Kringle4 and 5 of plasminogen linked to		
PT	B-chain of t-Pa or u-Pa via aminoacid sequence		
XX			
PS	Claim 11; Page 50; 64pp; English.		
CC	This hybrid plasminogen/u-Pa sequence is described in the		
CC	specification although the sequence itself is not given. The		
CC	sequence given here has been compiled using the human plasminogen		
CC	sequence from Patent No. WO9013640 and the human u-Pa sequence		
CC	from the SWISSPROT database (UROKSHUMAN). The hybrid fibrinolytic		
CC	enzymes are useful in the treatment of chromotic diseases.		
CC	See also R22899, R22502 and R22503.		
CC	(Updated on 09-JAN-2003 to add missing OS field.)		
SQ	Sequence 380 AA;		
Query Match	85.0%; Score 432; DB 13; Length 380;		
Best Local Similarity	82.6%; Pred.No.1,3e-34;		
Matches 71; Conservative	6; Mismatches 9; Indels 0; Gaps 0;		
OY	1 EODCMFNGSGYRGKKATVTGTPCOEAAQEPIRHSTFTPGTNKWGLEKNYCNPDPGD 60 :: :: :: :: :: :: :: :: :: :: :: :: 23 EDICMFNGSGYRKAKRTVGTGPDCDMAAEPIRHSIFETPNTPRAGLEKNYCNPDPGD 82 OY 61 INGWICYTMNPKLFDYCDIPLCASS 86 :::::::::: : Db 83 VGGFWCYTTMNRKLVDYCDVPQCPS 108 RESULT 5 AAR22503 ID AAR22503 standard; Protein; 476 AA. XX AAR22503; AC XX DT 09-JAN-2003 (updated) DT 25-AUG-1992 (first entry) XX [GRSRYQ]-[Plasminogen 347-541]-(u-Pa 137-411) hybrid. DE Plasminogen; urokinase-like plasminogen activator; hybrid; KM fibrinolysis; blood clotting; acute myocardial infarction. XX Homo sapiens. OS XX FH Key Location/Qualifiers EH Region 1..6 /note= "amino acids -3 to +3 of t-PA" FT FT Region 7..201 /note= "amino acids 347-541 of plasminogen" FT FT Region 202..476 /note= "amino acids 137-411 of u-PA" FT Cleavage-site 222..223 /note= "u-PA cleavage site"XX MO9204450-A. XX PN PD 19-MAR-1992. PF 29-AUG-1991; 91WO-GBO1455. PP PR 01-SEP-1990; 90GB-0019120. XX (BEC) BEECHAM GROUP PLC. XA		

PI Dodd I, Brown M, Robinson JH;
XX WPI, 1992-114357/14.
DR
XX Hybrid plasminogen activators for treating thrombotic diseases -
PT comprise Kringles 5 or Kringles 4 and 5 of plasminogen linked to
PT B-chain of t-PA or u-PA via aminoacid sequence
PS Claim 10; Page 50; 64pp; English.
XX
XX This hybrid plasminogen/u-PA sequence is described in the
CC specification although the sequence itself is not given. The
CC sequence given here has been compiled using the human plasminogen
CC sequence from Patent No. WO9013640 and the human u-PA sequence
CC from the SWISSPROT database (UROK\$HUMAN). The hybrid fibrinolytic
CC enzymes are useful in the treatment of thrombotic diseases.
CC See also R22499, R22502 and R22504.
CC (Updated on 09-JAN-2003 to add missing OS field.)
SQ Sequence 476 AA;
Query Match 85.0%; Score 432; DB 13; Length 476;
Best Local Similarity 82.6%; Pred. No. 1.7e-34;
Matches 71; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 1 EDDCMFNGNGKGYRKKATVTGTGTCOEWAQBPBHRSTFPGTNKAGLEKNCRNPDGD 60
DB 119 EDDCMFNGNGKGYRKKATVTGTGTCOEWAQBPBHRSTFPGTNKAGLEKNCRNPDGD 178
QY 61 INGPWCYTNNPRKLPDYCDIPLCASS 86
DB 179 VGGPWCYTNNPRKLPDYCDVPCPSS 204
RESULT 6
AAG67228
ID AAG67228 standard; Protein; 810 AA.
AC
XX AAG67228;
XX
XX 13-NOV-2001 (first entry)
DE Amino acid sequence of monkey plasminogen.
XX
XX Angiotatin; plasminogen; sulfhydryl donor; angiogenesis; tumour;
KW angiogenic disease; neoplastic disease; connective tissue disorder;
KW rheumatoid arthritis; atherosclerosis; ocular angiogenic disease;
KW diabetic retinopathy; corneal graft rejection; cardiovascular disease;
KW cerebral vascular disease; diabetes; immune disorder;
KW chronic inflammation; autoimmunity.
XX
XX Macaca mulatta.
OS
XX WO200158921-A2.
PN
XX 16-AUG-2001.
PD
XX 08-FEB-2001; 2001WO-US04021.
PF
XX 08-FEB-2000; 2000US-0500397.
PR
XX (NOUN) UNIV NORTHWESTERN.
PA
XX Soft G, Gately ST, Twardowski P;
PI WPI; 2001-550019/61.
DR
XX
XX Producing angiotatin for treating angiogenic diseases involves
PT contacting plasminogen with plasminogen activator and sulfhydryl donor
PT simultaneously, or producing plasmin which is contacted with sulfhydryl
PT donor
XX
XX Disclosure; Page 90-93; 101pp; English.

XX The specification describes a method for generating angiotatin in
CC vitro. The method comprises contacting plasminogen with a sulfhydryl
CC donor, or culturing cells capable of producing plasminogen activator
CC in conditioned culture medium (CCM) and contacting the CCM with
CC plasminogen. Angiotatin produced by method of the invention is useful
CC for treating animals with angiogenesis diseases. It is useful for
CC treating an angiogenic disease such as neoplastic diseases (e.g. tumours
CC and tumour metastasis), benign tumours (e.g. hemangiomas, acoustic
CC neuromas, etc), connective tissue disorders (e.g. rheumatoid arthritis
CC and atherosclerosis), ocular angiogenic diseases (e.g. diabetic
CC retinopathy, corneal graft rejection, etc), cardiovascular diseases,
CC cerebral vascular diseases, diabetes-associated diseases and immune
CC disorders (e.g. chronic inflammation and autoimmunity). The present
CC sequence represents a plasminogen.
SQ Sequence 810 AA;
Query Match 85.0%; Score 432; DB 22; Length 810;
Best Local Similarity 83.7%; Pred. No. 2.8e-34;
Matches 72; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 EDDCMFNGNGKGYRKKATVTGTGTCOEWAQBPBHRSTFPGTNKAGLEKNCRNPDGD 60
DB 478 EDDCMFNGNGKGYRKKATVTGTGTCOEWAQBPBHRSTFPGTNKAGLEKNCRNPDGD 537
QY 61 INGPWCYTNNPRKLPDYCDIPLCASS 86
DB 538 VGGPWCYTNNPRKLPDYCDVPCPSS 563
RESULT 7
AAB01914
ID AAB01914 standard; Protein; 90 AA.
AC
XX AAB01914;
XX
XX 18-SEP-2000 (first entry)
DE Human plasminogen kringles 5 (Val1454-Ala1543).
XX
XX Plasminogen; human; kringles domain; endothelial cell proliferation;
KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
KW antipsoriatic; antiinflammatory; anticancer; antirheumatic; antiarthritic;
KW antiangiogenic; cancer; tumour; autoimmune disease.
XX
XX Homo sapiens.
OS
XX US6057122-A.
PN
XX 02-MAY-2000.
PD
XX 05-MAY-1997; 97US-0851350.
PF
XX 03-MAY-1996; 96US-0643219.
PR
XX 03-APR-1997; 97US-0832087.
PA (ABBO) ABBOTT LAB.
PI
XX Davidson DJ;
PI
XX WPI; 2000-349573/30.
DR
XX
XX Preparation of Kringles five peptide fragment for treating various
PT disorders such as angiogenic, ocular, skin diseases and cancer.
PT involves mixing mammalian plasminogen and elastase followed by
PT incubation and isolation
XX
XX Example 17; Page -; 48pp; English.
PS
XX The invention relates to a method of preparing plasminogen kringles 5
CC peptide fragments. The method comprises mixing mammalian plasminogen and
CC elastase in the ratio 1:100-1:300, followed by incubating and isolating

CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
CC endothelial cell proliferation and migration. The peptides are useful
CC for treating angiogenic diseases, primary and metastatic solid tumours
CC and carcinomas of various organs such as breast, genital tract,
CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
CC arising from haematopoietic malignancies such as leukemias and
CC lymphomas. They are also used for the prophylaxis of various autoimmune
CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
CC Syndrome), diseases caused by excessive or abnormal stimulation of
CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
CC disease and ulcers). The peptides are also useful as a birth control
CC agent which inhibits ovulation and establishment of the placenta.
CC Sequences AAB01905-B01919 represent fragments of human plasminogen used
CC in an exemplification of the invention.
CC Note: This sequence is not shown in the specification, but is derived
CC from the full length human plasminogen sequence (AAB01887) shown in
CC figure 1.

SQ Sequence 90 AA;

Query Match 84.6%; Score 430; DB 21; Length 90;
Best Local Similarity 82.4%; Pred. No. 5.1e-35;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATVTGTPCQEWMAOEPHRHSFTFGTNKAGLEKNYCRNPDG 60
DB 6 EDDCMFGNGKGYRGKATVTGTPCQDWAQEPHRHSFTFGTNPRAGLEKNYCRNPDG 65
QY 61 INGPWCYTNNPRKLFDYCDIPLCAS 85
DB 66 VGGPWCYTNNPRKLYDCVPCQCA 90

RESULT 8
AAY58868

ID AAY58868 standard; Protein; 91 AA.

XX AAY58868;

DT 08-MAY-2000 (first entry)

DE Human plasminogen mature polypeptide.

XX Anti-angiogenic; angiogenesis inhibitor; cancer; tumour; therapy;

KW plasminogen; human.

XX Homo sapiens.

PN WO200004052-A2.

PD 27-JAN-2000.

PF 16-JUL-1999; 99WO-GB02292.

PR 16-JUL-1998; 98GB-0015505.

PA (ADPR-) ADPROTECH PLC.

PI Smith RAG, Bright JR, Steward M, Cox VF;

DR WPI; 2000-182406/16.

PT New soluble derivative of anti-angiogenic polypeptide useful for
PT treatment of primary or secondary cancers, contains covalently attached
PT membrane-binding elements for targeting -

PS Example 3; Page 21; 36pp; English.

XX The present sequence is that of human plasminogen mature
CC polypeptide. The invention relates to new soluble derivatives (I)
CC of anti-angiogenic polypeptides. (I) comprise 2 or more

CC heterologous membrane binding elements (MBEs, see AAY58855-61) with
CC low membrane affinity that are covalently attached to a soluble
CC anti-angiogenic polypeptide such as a non-catalytic region of human
CC plasminogen. The MBEs interact independently with thermodynamic
CC activity, with components of the vascular endothelium. (I)
CC provide targeted delivery of the anti-angiogenic polypeptide to
CC cell membranes and sites of active angiogenesis, particularly the
CC vascular endothelium, and therefore increase the local
CC concentration and reduce the risk of adverse effects on normal
CC processes elsewhere in the vasculature. They are used in a claimed
CC method of treatment of primary or secondary tumour.

SQ Sequence 91 AA;

Query Match 84.6%; Score 430; DB 21; Length 91;
Best Local Similarity 82.4%; Pred. No. 5.1e-35;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATVTGTPCQEWMAOEPHRHSFTFGTNKAGLEKNYCRNPDG 60
DB 2 EDDCMFGNGKGYRGKATVTGTPCQDWAQEPHRHSFTFGTNPRAGLEKNYCRNPDG 61
QY 61 INGPWCYTNNPRKLFDYCDIPLCAS 85
DB 62 VGGPWCYTNNPRKLYDCVPCQCA 86

RESULT 9

ID AAB01917 standard; Protein; 93 AA.

XX AAB01917;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 (Val154-Phe546).

XX Plasminogen; human; kringle domain; endothelial cell proliferation;

KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;

KW antiproliferative; antiinflammatory; antitumor; antineumatic; antiarteritic;

KW antiangiogenic; cancer; tumour; autoimmune disease.

XX Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

PA (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI; 2000-349573/30.

PT Preparation of Kringle five peptide fragment for treating various
PT disorders such as angiogenic, ocular, skin diseases and cancer,
PT involves mixing mammalian plasminogen and elastase followed by
PT incubation and isolation -

PS Example 17; Page -; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5
CC peptide fragments. The method comprises mixing mammalian plasminogen and
CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
CC endothelial cell proliferation and migration. The peptides are useful
CC for treating angiogenic diseases, primary and metastatic solid tumours
CC and carcinomas of various organs such as breast, genital tract,

XX The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g.: rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Weber syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human plasminogen used in an exemplification of the invention.

Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01887) shown in figure 1.

SQ	Sequence	98 AA;
	Query Match	84.6%; Score 430; DB 21; Length 98;
	Best Local Similarity	82.4%; Pred. No. 5,5e-35;
	Matches	70; Conservative 7; Mismatches 8; Indels 0; Gaps 0

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:
Dd 11 EEDCMFNGNGSGYRGKATTTVTGTPCQDMAQAQEPHRHSITPTPETNPRAGLEKNYCNPDPGD 70

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Qy      61  INGPWCYTMNPRLFDYCDIPLCA 85
      : ||||| ||||: |||:
Db      71  VGGPWCYTTNPRLYDYCDVPCAA 95
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RESULT 12

AAW34286
ID AAW34286 standard; protein; 101 AA

AC AAW34286;

DT 14-MAY-1998 (first entry)

DE Human kringling 5 peptide fragment.

KM Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
KM metastatic solid tumor; carcinoma; sarcoma; lymphoma; haemangioma;
KM psoriasis; arthritis; macular degeneration; diabetic retinopathy;
KM autoimmune diseases; ocular disease; capillary proliferation; therapy;
Kringle 5 receptor.

OS Homo sapiens.

PN W09741824-A2.

PD 13-NOV-1997.

PF 05-MAY-1997; 97WO-US07700.

PR 03-APR-1997; 97US-0832087.

XXXX

XX

PI Davidson DJ, Gubbins EJ, Wang J;

DR WPI; 1997-558670/51.

PT New kringle 5 peptide(s) and fusion proteins derived from

PT plasminogen - useful as anti-angiogenesis agents for treating
PT cancer, psoriasis, arthritis etc., including gene therapy
XX
PS Claim 35; Fig 2; 78pp; English.

PS Claim 35; Fig 2; 78pp; English.

This sequence is a kringle 5 (K5) peptide homologous to human plasminogen-K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangiomias. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The fragments can also be used to treat autoimmune or ocular diseases, capillary proliferation within atherosclerotic plaque, haemophilic joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantify the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothelial cells with low toxicity against normal cells. Typically they have 800-times greater inhibitory activity against bovine capillary cells in vitro than kringle 1-4 peptides.

XX	
SQ	Sequence 101 AA;
	Query Match 84.6%; Score 430; DB 18; Length 101;
	Best Local Similarity 82.4%; Pred.No. 5-7e-35;
Matches 70;	Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 17 BEDCFNNGCGYRGKATTVTGTGTCQDMAQEPHRHSFTPTETPRAGLEKNYCANPDGD 76

QY 61 INGPWCYTMNPKLFEDYCDIPLCAS 85
: ||||| ||||: |||: |||:
Db 77 VGGPWCYTTNPKLYDYCDVPQCAA 101

RESULT 1

ID AAB01890 standard; Protein; 101 AA.

AC AAB01890;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5, SEQ ID NO:34.

KM plasminogen, kringle 5 domain; endothelial cell proliferation;
KM angiogenesis; antiproliferative; antiatherosclerotic; cytostatic;
KM antipapillary; antinflammatory; anticancer; antineoplastic; antichronic;
KM antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350

PR 03-MAY-1996; 96US-0643219

XX

PA (ABBO) ABBOTI LAB.

Davidson DJ ;

DR WPI; 2000-349573/30.

PA (ABBO) ABBOTT LAB.
 XX
 PI Davidson DJ;
 XX

DR WPI, 2000-349573/30.
 XX

PT Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -

XX
 PS Example 17; Page -; 48pp; English.
 XX

CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Weber
 CC Syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived
 CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.
 XX
 XX

SQ Sequence 104 AA;

Query Match 84.6%; Score 430; DB 21; Length 104;

Best Local Similarity 82.4%; Pred. No. 5.9e-35;
 Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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 DB 17 EEDCMFGNGKGYRGKATVTGTGTCOAWAQBPHRSTFIPTNPRAGLEKXNCRNPDGD 76

QY 61 INGPWCYTNNPRKLPDYCDIPICAS 85
 DB 77 VGGPWCYTNNPRKLPDYCDVPCOCAA 101

Search completed: January 12, 2004, 17:23:22
 Job time : 35.2707 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:24:03 ; Search time 25.218 Seconds
(without alignments)
687.200 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	508	100.0	91	US-09-748-468-1 Sequence 1, Appli
2	508	100.0	1169	US-09-870-759-126 Sequence 126, App
3	508	100.0	1169	US-09-751-708A-126 Sequence 126, App
4	430	84.6	791	US-09-967-386-1 Sequence 1, Appli
5	430	84.6	791	US-10-304-287-1 Sequence 1, Appli
6	430	84.6	810	US-09-946-893-2 Sequence 2, Appli
7	430	84.6	810	US-10-137-144-1 Sequence 1, Appli
8	430	84.6	810	US-10-193-656-2 Sequence 1, Appli
9	427	84.1	569	US-09-946-893-5 Sequence 5, Appli
10	427	84.1	571	US-09-946-893-8 Sequence 8, Appli
11	427	84.1	576	US-09-946-893-6 Sequence 6, Appli
12	425	83.7	458	US-09-946-893-4 Sequence 4, Appli
13	412	81.1	80	US-09-753-064-6 Sequence 6, Appli
14	412	81.1	80	US-10-267-137-8 Sequence 8, Appli
15	406	79.9	812	US-09-788-142-1 Sequence 1, Appli

16	406	79.9	812	9	US-09-761-120-1	Sequence 1, Appli
17	406	79.9 <td>812</td> <td>9<th>US-09-873-676-81</th><th>Sequence 81, Appli</th></td>	812	9 <th>US-09-873-676-81</th> <th>Sequence 81, Appli</th>	US-09-873-676-81	Sequence 81, Appli
18	406	79.9 <td>812</td> <td>10<th>US-09-335-325-1</th><th>Sequence 1, Appli</th></td>	812	10 <th>US-09-335-325-1</th> <th>Sequence 1, Appli</th>	US-09-335-325-1	Sequence 1, Appli
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28	276.5	54.4	339	9 <th>US-09-335-325-4</th> <th>Sequence 4, Appli</th>	US-09-335-325-4	Sequence 4, Appli
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30	276.5	54.4	339	15 <th>US-10-131-241-4</th> <th>Sequence 4, Appli</th>	US-10-131-241-4	Sequence 4, Appli
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32	274.5	54.0	79	10 <th>US-09-335-325-9</th> <th>Sequence 9, Appli</th>	US-09-335-325-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-09-748-468-1
; Sequence 1, Application US/09748468
; Patent No. US20010051347A1
; GENERAL INFORMATION:
; APPLICANT: Kundu, S.
; TITLE OF INVENTION: SPECIFIC ANTIBODIES TO KININASE 5 OF
; TITLE OF INVENTION: APO(A) AND METHODS OF USE THEREFOR
; FILE REFERENCE: 6296 US, 01
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: 09/234, 553
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 91
; ORGANISM: Homo sapiens
US-09-748-468-1

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QY 1 EODCMFGNGKGRGKATTVGTGPOEAAOEPHRSFIFGTKKMAGLEKNYCRNPGD 60
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QY 61 INGPWCYTMNPKLFDYCDIPLCASS 86
DB 63 INGPWCYTMNPKLFDYCDIPLCASS 88

RESULT 2
US-09-870-759-126
; Sequence 126, Application US/09870759

Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-126

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RESULT 3
US-09-751-708A-126
; Sequence 126, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-708A-126

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Qy 61 INGPWCYTNNPRLFDYCDIPLCASS 86
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RESULT 4
US-09-967-386-1
; Sequence 1, Application US/09967386
; Patent No. US20020159992A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Henkin, Jack
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
; TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS

FILE REFERENCE: 6738.US.02
; CURRENT APPLICATION NUMBER: US/09/967,386
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/236,550
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-967-386-1

Query Match
Best Local Similarity 84.6%; Score 430; DB 10; Length 791;
Best Local Similarity 82.4%; Pred. No. 1,1e-39;
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Qy 61 INGPWCYTNNPRLFDYCDIPLCASS 85
Db 519 VGGPWCYTNNPRLFDYCDIPLCASS 543

RESULT 5
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; Sequence 1, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; APPLICANT: Kwon, MiJung
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
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; LENGTH: 791
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US-10-304-287-1

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; Sequence 2, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Inhibitors
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05

Patent No. US20020072494A1
GENERAL INFORMATION:

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; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Newburn
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
; OTHER INFORMATION: with a tumor targeting signal peptide
; US-09-946-893-8

Query Match      84.1%; Score 427; DB 9; Length 571;
Best Local Similarity 80.2%; Pred. No. 1.7e-39;
Matches 69; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSFTPGTNKWALEKXNCRNPDG 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 EEDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSFTPETNPRAGLEKXNCRNPDG 537
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 INGPWCYTNNPRKLFYDCDIPLCASS 86
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 538 VGGPWCYTNNPRKLYDYCDVPOCCAA 563
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
; US-09-946-893-6
; Sequence 6, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Newburn
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
; OTHER INFORMATION: with a tumor targeting signal
; US-09-946-893-6

Query Match      84.1%; Score 427; DB 9; Length 576;
Best Local Similarity 80.2%; Pred. No. 1.7e-39;
Matches 69; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSFTPGTNKWALEKXNCRNPDG 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 EEDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSFTPETNPRAGLEKXNCRNPDG 537
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 INGPWCYTNNPRKLFYDCDIPLCASS 86
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 538 VGGPWCYTNNPRKLYDYCDVPOCCAA 563
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
; US-09-946-893-4
; Sequence 4, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Newburn
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-946-893-4

Query Match      83.7%; Score 425; DB 9; Length 458;
Best Local Similarity 83.1%; Pred. No. 2.3e-39;
Matches 69; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSFTPGTNKWALEKXNCRNPDG 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 376 EEDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSFTPETNPRAGLEKXNCRNPDG 435
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 INGPWCYTNNPRKLFYDCDIPLC 83
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 436 VGGPWCYTNNPRKLYDYCDVPOC 458
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
; US-09-753-064-6
; Sequence 6, Application US/09753064
; Patent No. US2001001644A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/753,064
; FILING DATE: 29-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/763,528
; FILING DATE: 12-Dec-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; REFERENCE/DOCKET NUMBER: 05940-0251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
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ANTI-SENSE: NO
FRAGMENT TYPE: Internal
FEATURES:
NAME/KEY: Protein
LOCATION: 1..80
OTHER INFORMATION: /note="Kringle 5 - Figure 3"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-753-064-6

Query Match 81.1%; Score 412; DB 9; Length 80;
Best Local Similarity 83.8%; Pred. No. 9.8e-39;
Matches 67; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 4 CMFGNGKGYRGKATVTGTPCOEWAQEPHRSFTIPGNTKMAGLEKXKNCNPDGDD 63
Db 1 CMFGNGKGYRGKATVTGTPCOEWAQEPHRSFTIPGNTKMAGLEKXKNCNPDGDD 60
64 PWCYTNPRKLPDYCDIPLC 83
Db 61 PWCYTNPRKLPDYCDVPOC 80

RESULT 14
US-10-267-137-8
Sequence 8, Application US/10267137
Publication No. US20030148950A1
GENERAL INFORMATION:
APPLICANT: Xin, Li
APPLICANT: Li, Zai-Ping
APPLICANT: Gan, Ren-bao
APPLICANT: Zhou, Qing-wei
APPLICANT: Xu, Ren
TITLE OF INVENTION: KRINGLE DOMAIN 1 OF HUMAN HEPATOCTE
FILE REFERENCE: GROWTH FACTOR AND USES THEREFOR
CURRENT APPLICATION NUMBER: US/10/267,137
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/328,329
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 80
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Sequence alignment of kringle domains of
US-10-267-137-8

Query Match 81.1%; Score 412; DB 12; Length 80;
Best Local Similarity 83.8%; Pred. No. 9.8e-39;
Matches 67; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 4 CMFGNGKGYRGKATVTGTPCOEWAQEPHRSFTIPGNTKMAGLEKXKNCNPDGDD 63
Db 1 CMFGNGKGYRGKATVTGTPCOEWAQEPHRSFTIPGNTKMAGLEKXKNCNPDGDD 60
64 PWCYTNPRKLPDYCDIPLC 83
Db 61 PWCYTNPRKLPDYCDVPOC 80

RESULT 15
US-09-788-142-1
Sequence 1, Application US/09788142
Patent No. US20010029246A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Akeew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/788,142
FILING DATE: 16-Feb-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/866,735
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Murine
IMMEDIATE SOURCE:
CLONE: Plasmidogen
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-788-142-1

Query Match 79.9%; Score 406; DB 9; Length 812;
Best Local Similarity 79.1%; Pred. No. 5.7e-37;
Matches 68; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 1 EDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSFTIPGNTKMAGLEKXKNCNPDGDD 60
Db 478 EDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSFTIPGNTKMAGLEKXKNCNPDGDD 537
61 INGPWCYTNPRKLPDYCDIPLC 86
Db 538 INGPWCYTNPRKLPDYCDIPLC 86

Search completed: January 12, 2004, 17:29:39
Job time : 25.218 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 17:21:34 ; Search time 12.2857 Seconds
(without alignments)
296.176 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508
Sequence: 1 EDDCMFGNGKGYRGKATTV.....YTMNPKLFYDCDIPLCASS 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
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- 6: /cgn2_6/prodata/1/1aa/5D_COMB.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	91	3	US-09-234-553-1
2	432	85.0	810	4	US-08-991-761A-11
3	430	84.6	90	2	US-09-131-995-4
4	430	84.6	90	2	US-08-832-087B-4
5	430	84.6	90	3	US-09-132-154-4
6	430	84.6	93	2	US-09-131-995-7
7	430	84.6	93	2	US-08-832-087B-7
8	430	84.6	93	2	US-09-132-154-7
9	430	84.6	95	2	US-09-131-995-3
10	430	84.6	95	2	US-08-832-087B-3
11	430	84.6	95	2	US-09-132-154-3
12	430	84.6	98	2	US-09-131-995-6
13	430	84.6	98	2	US-08-832-087B-6
14	430	84.6	98	2	US-09-132-154-6
15	430	84.6	101	2	US-09-131-995-2
16	430	84.6	101	2	US-08-832-087B-2
17	430	84.6	101	3	US-08-851-350-34
18	430	84.6	101	3	US-09-132-154-2
19	430	84.6	104	2	US-09-131-995-5
20	430	84.6	104	2	US-08-832-087B-5
21	430	84.6	104	3	US-09-132-154-5
22	430	84.6	790	1	US-08-469-486-54
23	430	84.6	790	2	US-08-469-658-54
24	430	84.6	791	2	US-09-131-995-1
25	430	84.6	791	2	US-08-832-087B-1
26	430	84.6	791	3	US-09-132-154-1
27	430	84.6	791	4	US-08-991-761A-6

28	430	84.6	810	1	US-07-854-603-2	Sequence 2, Appli
29	430	84.6	810	1	US-08-147-000B-29	Sequence 29, Appli
30	430	84.6	810	3	US-09-086-514-1	Sequence 1, Appli
31	430	84.6	810	4	US-09-192-012-5	Sequence 5, Appli
32	430	84.6	810	6	5200340-8	Patent No. 5200340
33	430	84.6	814	1	US-08-750-711-1	Sequence 1, Appli
34	428	84.3	101	3	US-08-851-350-36	Sequence 36, Appli
35	425	83.7	90	1	US-08-643-219-4	Sequence 8, Appli
36	425	83.7	93	1	US-08-643-219-7	Sequence 7, Appli
37	425	83.7	95	1	US-08-643-219-3	Sequence 3, Appli
38	425	83.7	98	1	US-08-643-219-6	Sequence 6, Appli
39	425	83.7	101	1	US-08-643-219-2	Sequence 2, Appli
40	425	83.7	104	1	US-08-643-219-5	Sequence 5, Appli
41	425	83.7	333	4	US-08-991-761A-8	Sequence 8, Appli
42	425	83.7	791	1	US-08-643-219-1	Sequence 1, Appli
43	425	83.7	791	3	US-08-851-350-1	Sequence 1, Appli
44	419	82.5	100	1	US-08-643-219-9	Sequence 9, Appli
45	419	82.5	100	2	US-09-131-995-9	Sequence 9, Appli

ALIGNMENTS

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RESULT 1
US-09-234-553-1
; Sequence 1, Application US/09234553
; Patent No. 6210906
; GENERAL INFORMATION:
; APPLICANT: Kundu, S.
; TITLE OF INVENTION: SPECIFIC ANTIBODIES TO KRINGLE 5 OF
; FILE REFERENCE: 6296 US 01
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-234-553-1

Query Match      100.0%; Score 508; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTVGTGQEWAAQEPHRSHTFIPGTNKMAGLEKNYCRNPDGD 60
DB 3 EDDCMFGNGKGYRGKATTVGTGQEWAAQEPHRSHTFIPGTNKMAGLEKNYCRNPDGD 62
QY 61 INGPWCYTMRPKLFYDCDIPLCASS 86
DB 63 INGPWCYTMRPKLFYDCDIPLCASS 88

RESULT 2
US-08-991-761A-11
; Sequence 11, Application US/08991761A
; Patent No. 6576609
; GENERAL INFORMATION:
; APPLICANT: Goff, Gerald
; APPLICANT: Gately, Stephen
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: "Methods and Compositions for Generating
; TITLE OF INVENTION: "Angiostatin"
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
```

```

? ZIP: 80203
? COMPUTER READABLE FORM:
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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/991,761A
? FILING DATE:
? CLASSIFICATION: 1642
? ATTORNEY/AGENT INFORMATION:
? NAME: Crook, Wannell M.
? REGISTRATION NUMBER: 31,071
? REFERENCE/DOCKET NUMBER: 3501-16-1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (303) 863-9700
? TELEFAX: (303) 863-0223
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 810 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-991-761A-11

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Query Match	85.0%	Score 432;	DB 4;	length 810;
Best Local Similarity	83.7%	Pred. No. 6,8e-41;		
Matches 72;	Conservative 4;	Mismatches 10;	Indels 0;	Gaps 0

Dy 1 EDDCFGNGSGYRGKATTTVTGTPCQEWAAQEPHRHSIFIPGNKKMAGLSEKNYCRRPDGD 60
:
Db 478 EEDCFGNGSGYRGKATTTVTGTPCQEWAAQEPHSHRIFTPEINPRAGLEKNYCRRPDGD 53

Qy	Db
61	INGPWCYTMNPKLFDYCDIPICASS 86
:	: :
538	VGGPWCYTTNPKLFDYCDVPQCAAS 563

RESULT 3
 US-09-131-995-4
 : Sequence 4, Application US/09131995
 : Patent No. 5972896
 : GENERAL INFORMATION:
 : APPLICANT: Davidson, Donald J.
 : TITLE OF INVENTION: NOVEL ANTANGIOGENIC PEPTIDES
 : TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
 : NUMBER OF SEQUENCES: 14
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Abbott Laboratories
 : STREET: 100 Abbott Park Road
 : CITY: Abbott Park
 : STATE: IL
 : COUNTRY: USA
 : ZIP: 60064
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/131,995
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/08/632,087
 : FILING DATE: 03-APR-1997
 : APPLICATION NUMBER: 08/643,219
 : FILING DATE: 06-MAY-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Casauto, Diane
 : REGISTRATION NUMBER: 40,943
 : REFERENCE/DOCKET NUMBER: 5940.US..P1

```

? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 847-938-3137
? TELEFAX: 847-938-2623
?
? TELEX:
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 90 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE:
? DESCRIPTION: protein
? FRAGMENT TYPE: internal
?
US-09-131-995-4

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Query Match	84.6%	Score 430; DB 2;	length 90;
Best local Similarity	82.4%	Pred. No. 1,6e-42;	
Matches 70; Conservative	7;	Mismatches 8;	Indels 0; Gaps 0;

QY 1 EQDCMFGNGSGYRGKATTTGTGTCQEMAQAEHRHSFTIPGTHKMAGLEKNYCSRPDGD 60

DB 6 EBDCMFGNGSGYRGKATTTGTGTCQDMAQAEHRHSFTIPETNPRAGLEKNYCSRPDGD 65

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QY      61  INGPWCYTNNPRKLFYDCIDPLCAS  85
      : ||||| : ||| : || :
DB      66  VGGPWCYTNNPRKLYDCDVPQCAA  90

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RESULT 4
US-08-832-087B-4
; Sequence 4, Application US/08832087B

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1  /  INVENTION:
2  /
3  /  GENERAL INFORMATION:
4  /
5  /  APPLICANT:  Davidson, Donald J.
6  /
7  /  TITLE OF INVENTION:  NOVEL ANTIANGIOGENIC PEPTIDES
8  /

```

TITLE OF INVENTION:
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories

/ SINGER: 100 Abbott Park
 /
 / CITY: Abbott Park
 /
 / STATE: IL
 /
 / COUNTRY: USA
 /

```

; ZIF: 00004
;
; COMPUTER READABLE FORM
;
; MEDIUM TYPE: Disket
;
; COMPUTER: IBM Compat
;

```

```

; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832.087B
;

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; FILING DATE: 03-APR-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/643,219

; FILING DATE: 06-MAY-1996
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Casuto, Dianne
 ; REGISTRATION NUMBER: 40 943

REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-838-2623

```

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; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE:
;      SUBSTRUCTURE:

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FRAGMENT TYPE: internal
US-08-832-087B-4

Query Match 84.6%; Score 430; DB 2; Length 90;
Best Local Similarity 82.4%; Pred. No. 9.6e-42;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTTGTGTCOEWAQEPHRSHTFTGTNKGAGLEKXKNCNPDGD 60
DB 6 EEDCMFGNGKGYRGKATTTGTGTCOEWAQEPHRSHTFTGTNKGAGLEKXKNCNPDGD 65
QY 61 INGPWCYTNNPRKLFYCDIPICAS 85
DB 66 VGGPWCYTNNPRKLYDYCDVPQCAA 90

RESULT 5
US-09-132-154-4
Sequence 4, Application US/09132154

Patent No. 6251867
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/132,154
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
DESCRIPTION: internal
FRAGMENT TYPE: internal
US-09-132-154-4

Query Match 84.6%; Score 430; DB 3; Length 90;
Best Local Similarity 82.4%; Pred. No. 9.6e-42;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTTGTGTCOEWAQEPHRSHTFTGTNKGAGLEKXKNCNPDGD 60
DB 6 EEDCMFGNGKGYRGKATTTGTGTCOEWAQEPHRSHTFTGTNKGAGLEKXKNCNPDGD 65
QY 61 INGPWCYTNNPRKLFYCDIPICAS 85
DB 66 VGGPWCYTNNPRKLYDYCDVPQCAA 90

RESULT 6
US-09-131-995-7
Sequence 7, Application US/09131995

Patent No. 5972896
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
DESCRIPTION: internal
FRAGMENT TYPE: internal
US-09-131-995-7

Query Match 84.6%; Score 430; DB 2; Length 93;
Best Local Similarity 82.4%; Pred. No. 9.9e-42;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTTGTGTCOEWAQEPHRSHTFTGTNKGAGLEKXKNCNPDGD 60
DB 6 EEDCMFGNGKGYRGKATTTGTGTCOEWAQEPHRSHTFTGTNKGAGLEKXKNCNPDGD 65
QY 61 INGPWCYTNNPRKLFYCDIPICAS 85
DB 66 VGGPWCYTNNPRKLYDYCDVPQCAA 90

RESULT 7
US-08-832-087B-7
Sequence 7, Application US/08832087B

Patent No. 5981484
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087B
FILING DATE: 03-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
FRAGMENT TYPE: internal
US-08-832-087B-7

Query Match 84.6%; Score 430; DB 2; Length 93;
Best Local Similarity 82.4%; Pred. No. 9.9e-42;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFNGKGYRGKATVTGTPCOEAAOEPHRSTFIPGNNKAGLEKXNCRRPDGD 60
DB 6 EDDCMFNGKGYRGKATVTGTPCOEAAOEPHRSTFIPGNNKAGLEKXNCRRPDGD 65

QY 61 INGPWCYTNNPRKLPDYCDIPLCAS 85
DB 66 VGGPWCYTNNPRKLPDYCDVPCQCA 90

RESULT 8
US-09-132-154-7
Sequence 7, Application US/09132154
Patent No. 6251867
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/132,154
FILING DATE:
TELECOMMUNICATION INFORMATION:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
FRAGMENT TYPE: internal
US-09-132-154-7

Query Match 84.6%; Score 430; DB 3; Length 93;
Best Local Similarity 82.4%; Pred. No. 9.9e-42;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFNGKGYRGKATVTGTPCOEAAOEPHRSTFIPGNNKAGLEKXNCRRPDGD 60
DB 6 EDDCMFNGKGYRGKATVTGTPCOEAAOEPHRSTFIPGNNKAGLEKXNCRRPDGD 65

QY 61 INGPWCYTNNPRKLPDYCDIPLCAS 85
DB 66 VGGPWCYTNNPRKLPDYCDVPCQCA 90

RESULT 9
US-09-131-995-3
Sequence 3, Application US/09131995
Patent No. 5972896
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623

[illegible]

APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: internal
FRAGMENT TYPE: internal
US-09-132-154-6

Query Match 84.6%; Score 430; DB 3; Length 98;
Best Local Similarity 82.4%; Pred. No. 1,1e-41;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EDDCMFGNGKGYRGKRAATVTGTGTCQEWAAQEPHRSFTIPGINKWAGLEKNYCRNPDD 60
Db 11 EDDCMFGNGKGYRGKRAATVTGTGTCQEWAAQEPHRSFTIPGINKWAGLEKNYCRNPDD 70
Qy 61 INGPWCYTNMPKRLFDYCDIPLCAS 85
Db 71 VGGPWCYTNMPKRLYDPCVPCAA 95

RESULT 15

US-09-131-995-2
Sequence 2, Application US/09131995
Patent No. 5972896
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: internal
FRAGMENT TYPE: internal
US-09-131-995-2

Query Match 84.6%; Score 430; DB 2; Length 101;
Best Local Similarity 82.4%; Pred. No. 1,1e-41;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EDDCMFGNGKGYRGKRAATVTGTGTCQEWAAQEPHRSFTIPGINKWAGLEKNYCRNPDD 60
Db 17 EDDCMFGNGKGYRGKRAATVTGTGTCQEWAAQEPHRSFTIPGINKWAGLEKNYCRNPDD 76
Qy 61 INGPWCYTNMPKRLFDYCDIPLCAS 85
Db 77 VGGPWCYTNMPKRLYDPCVPCAA 101

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Job time : 13.2857 secs

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